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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

REFERENCE

AUTHORS JOURNAL

Kim,K., Peters-Wendisch,P.G.,
Unpublished
2 (bases 1 to 2123)

REFERENCE

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Y17592.1 GI:14572581
accDA gene; acety1-CoA carboxylase; carboxyltransferase.
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Corynebacteriaceae; Corynebacterium

Sahm, H. and Eikmanns, B.J.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 CGL17592 LOCUS Result No. a იი O a 0000 0 0 0 O 00000 a a 38 39 40 142 140.6 132.6 132.6 132.6 133.1 131 131 132.8 122.8 122.8 122.2 120.2 120.2 120.2 120.2 120.2 120.2 120.3 120.4 148.6 691.4 515 312.6 312.6 312.6 Score 1473 1473 1575 2123 bp DNA Corynebacterium glutamicum accDA gene. Y17592 32.6 300750 24.3 3013 14.7 17910 14.7 37650 14.7 342300 7.7 342300 7.5 10029 7.4 10029 7.0 260050 6.7 36063 6.6 289900 6.2 294250 100.0 59.4 69.4 Match 6.2 354 6.0 7697 6.0 9508 5.9 6908 5.8 11976 5.8 11976 5.7 304454 5.7 31045 5.7 31045 5.7 3105 5.7 3105 5.6 1037 5.6 301200 5.6 301200 5.6 301200 5.6 301200 5.6 301200 5.6 301200 5.6 301200 5.7 31369 5.6 301200 5.6 301200 5.6 301200 5.6 301200 5.6 301200 5.7 301200 5.6 301200 332050 349980 1575 1473 Length B AE014498 SME591782 MLU15184 AP003005 AP0005937 AP001557 AP012526 BD165643 AE007944 AE008976 AE001231 AE004735 AE001231 AE001231 AE001236 AE012365 AE0123661 AE0124030 AE0124030 AE014030 BX248337 MLEPRTN8 AE009634 CGGLTG AE006979 MTCY31 CGL17592 AR202319 BD004741 AR202320 AX121013 BD004742 BD163130 AP005217 AP005276 AX127145 AX066443 ALIGNMENTS linear AE009634 Brucella AE014498 Brucella AE014498 Brucella AL591782 Sinorhizo U15184 Mycobacteri AP003005 Mesorhizo AP00397 Bradyrhiz AP001517 Bacillus AX123526 Sequence BD165643 Novel pol AE007944 Agrobacte AE008976 Agrobacte L59237 Synethococc AB031231 Pseudomon AE004735 Pseudomon AE001518 Helicobac AE016956 Enterococ AE012365 Xanthomon AP005276 Corynebac AX127145 Sequence AX066443 Sequence AR202320 Sequence AX121013 Sequence BD004742 Replicabl BD163130 Novel pol AP005217 Corynebac AP005217 Corynebac X66112 C.glutamicu AE006979 Mycobacte Z73101 Mycobacteri AE000604 AF139661 AL162754 BD092453 BX248337 Mycobacte AL583924 Mycobacte AR202319 Sequence BD004741 Replicabl Y17592 Corynebacte Description BCT 26-JUN-2001 Helicobac Azospiril Bacillus Thermosyn Xanthomon Neisseria Identific Sequence Bacillus Caulobact Deinococc Neisseria Pseudomon

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481 ATTAATTAACAAAGCCATTTTTCGGCCGTGGAGAAGCGTTTTCCGACTATGGTGTGGGGC 540 	421 TCGATAGCCTAAATTGGGCTTAGATCTTCCGCCTCTAAATAGGTATGCAGAGACATTCGA 480	361 ACGTCTAGGCAAAAAGTAGTTTTGTGAGATGAAACGCATAATCCGTCATTTTTTACGCAA 420 	301 GTGCAATAGTTAACGGGCTTCACACGTCACCATTCTGTCCGGTTTTTAGGCTATGTTCGGG 360	241 TCCCGATCTACCCCCCTCTTTACCCCGAAATACCCCTTTTGCAAAGATTGCAAACACAACA 300 	181 ACTCCCCCAATATCTTAACTTAAACTTAAAAGTAGTGTTTTACCTGCATTTATAAAAGT 240 	121 AACGTGTGAAGTGAAGTTACCTAACTCACATTGCAATGCGATAGCGATTTGGAAAACTC 180	61 CTTATATGTTTCTCACCACATCTGGCCGACGACGACGAGTATGTTGTCGATCACAGCTA 120	1 CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA 60 	Query Match 100.0%; Score 2123; DB 1; Length 2123; Best Local Similarity 100.0%; Pred. No. 0; Matches 2123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	LPADLVYAARNAWLSALPPEGASAILERDTNHAABIIERQGVQAHALLSQGLIDGIVA ETEHFVEEILGTISNALSELDNNPERAGRDSRFTRFERLAQ" 460 a 574 c 592 g 497 t	AMASWGSSGHLTFAEBGAQIGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSP LQLBAAVAKTLKVIQPVEATDRFSPTTPGVALLPVMEALARSRDÞQRFGIGEIMETLGA DVVKLSGARAGALSPAVRVALARIGGRPVVLIGQDRRFTLGPQELRFARRGISLAREL NLPIVSIIDTSGAELSQAAEBLGIASSIARTLSKLIDAÞLÞTVSVIIGQOVGGALAM	/db_xref="gI:14572582" /translation="MEKRFPIMVWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQ /translation="MEKRFPIMVWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQ GYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIH RATELKLPLLVSPASGGARMOEDNRAFVMMVSITAAVORHREAHLPELYVLRNTMGG	<pre>/transT_table=11 /product="putative carboxyltransferase subunit of acetyl-CoA carboxylase" /profein id="CAC42827 1"</pre>	508. 1983	130; on:17		Related sequence x66112. Recation/Qualifiers	endisch, P.G. ubmission d (17-JUN-1998)	
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Query Natcher Oy Db Db Db Db Db	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE BASE COUNT ORIGIN	RESULT 2 AR202319 LOCUS DEFINITION ACCESSION VERSION KEYMORDS SOURCE	8 8 8 8 8 B	\$
Query Match 100.0%; Score 2123; DB 6; Length 2123; Best Local Similarity 100.0%; Pred. No. 0; Matches 2123; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA 60	Tilg,Y., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel,B. Tilg,Y., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel,B. Process for the preparation of L-amino acids by fermentation and nucleotide sequences coding for the accDA gene nucleotide sequences coding for the accDA gene Patent: US 6361986-A 1 26-MAR-2002; Location/Qualifiers 1. 2123 ce /organism="unknown" 1. 460 a 574 c 592 g 497 t	loi dccdaccrrcardccrrdaArrc 2123 AR202319 Sequence 1 from patent US 6361986. AR202319 AR202319 AR202319.1 GI:20256858	AACAATCCGGAGAGGGGGACGCGACAGTCGCTTCACAGGATTTGAGCGTTTAGCGCAG 1980 TAAAGAAAATTATGCGCTGATCAAATCGATGATGACACCAGGGTTTGAGCGCAGACAGTGG 2040 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1621 GCTCCCCTCCCCACCGTTTCGGTCATTATTGGTCAGGGGGTTGGCGGTGGCGCTTGGCC 1680 1681 ATGCTGCCCGCCGATCTGGTCTACGCGGCGAAAACGCGTTGGCGGTTGGCGCTTGCCCACCC, 1740 1681 ATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTTGGCGATTGCCACCC, 1740 1681 ATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTTGGCGATTGCCACCC, 1740 1681 ATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTTGCCGCATTGCCACCC, 1740 1741 GAGGGCCCTCGGCCATCCTCTTCCGCGACACCAACCAACC
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Replicable DNA, amino acid sequence, Corynebacterium microorg shuttle vector, and process for producing L-amino acid. BD004741. GI:18632702 JP 2001008693-A/1. Corynebacterium glutamicum Corynebacterium glutamicum Bacteria, Actinobacteria, Actinobacteria, Actinobacteria, Corynebacterium.
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RS Tilke,I., Eggering,L., Eickmans,B., Zamu,H. and Meck,V.

Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector, and process for producing L-amino acid

AL Patent: JP 200108693-A, 1 16-JAN-2001;
DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH

OS COrynebacterium glutamicum

PN JP 2001008693-A/1

PD 16-JAN-2000 JP 2000153547

PF 27-MAY-2000 JP 2000153547

PF 27-MAY-1999 DE 19924365.4

PI VETYNA MECKEL

PC C12N15/09,C12N1/21,C12P13/04,C12P13/06,C12P13/06,C12P13/08, PC

C12P13/08,
PC C12P13/12,C12P13/20,C12P21/02//(C12N15/09,C12R1:15),(C12N1/21,DC)

PC C12P13/12,C12P13/20,C12P21/02//(C12N15/09,C12R1:15),(C12N1/21,DC)
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PC C12R1:15),
PC (C12R1:15),
(C12P13/04, C12R1:15), (C12P13/06, C12R1:15), (C12P13/08, C12R1:15), P.
(C12P13/12, C12R1:15), (C12P13/20, C12R1:15), (C12P21/02, C12R1:15),
C12N15/00,
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Pred. No. 0;
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	1501 CGCGAGCTAAACCTGCCGATCGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAG 1560 	
FEATURES source	1441 CGCCGCTTCACGCTTGGGCCGCAGGAGCTGGCTTTTTGCGTGGCATTTTCGCTGGCG 1500	•
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REFERENCE 1 AUTHORS Nakagawa,	1261 GTGATGGAGGCGATTGCGCGTTCTCGTGACCCGCAGAGGCCTGGAATCGGGGGAGATTATG 1320 	• •
KEYWOODS SOURCE Corynebact ORGANISM Corynebact Bacteria;	1201 ATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACTCCTGGCGTGGCACTTCCG 1260	
JOSEPH APOSTON	1141 ATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTT 1200 	
RESULT 4 APO05276/c APO05276 APO05276 COCUS APO05276	1081 ACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGGTGAAAACTGGTGTG 1140 	
Db 2101 GCGACC	1021 ACTITTGCGGAACCCGGCGGCAGATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACC 1080	
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TTCATGCCTGGAATTC
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d (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co. kyo Research Laboratories; 3-6-6, Asahi-machi, Machida, '4-8533, Japan (E-mail:snakagawa@xanagen.com, '4-829-3031, Fax.81-44-813-1651) puence is conducted by collaboration of Kyowa Hakko Kogy And Kitasato University. cterium glutamicum ATCC 13032 cterium glutamicum ATCC 13032 ; Actinobacteria, Actinobacteridae, Actinomycetales, genomic sequence hed 332050 bp DNA Cterium glutamicum ATCC 13032 DNA, /gene="Cg10654" 314. .2518 /gene="Cg10654" /note="PF02554:Carbon starvation protein CstA" **3 1 to 332050)** Š cterineae; Corynebacteriaceae; Corynebacterium BA000036 .1 GI:21323419 ubmission /organism="Corynebacterium /mol_type="genomic DNA" /strain="ATCC 13032" Location/Qualifiers
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SVGASKSPRIFGEFSTLAADFRELENSADDADFTADFRRLTSKEDDLVAANTHNQFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (8265. .8987)
/gene="Cgl0662"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVVLPMAGHKGYAISFMMDVLSGVLTGSQHSTKVHGPYDPTPPGGAGHLFIALDVAAF
RDPQDFDDALSDLVGEVKSTPKAQNTEEIFYPGESEDRAHRKNSAHGISLPEKTWMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MPEVTVNAQQLTVLCTDILTKTGVPAADALVGDSLVQADLWGH
PSHGYLRLPWYVRRLHSGAWTTHAHVEVLNDLGAVLALDGHRGIGQVLADHARKEAVT
RAMMFGIGAVSVRNSKHFGTAMYYTRKAAAQGCVSILTINASPAMAPWGGREKKIGTN
PWSIAAPFGETATVVDIANTAVARGKIYHARQTNMPIPETWAITSEGAPTTDPAEAIN
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DFFTPLFVIARVAGWTAHIVEQYENNSLIRPLSEYNGEEQREVAPIEKR"
                                                                                                                                                                  complement (9094. .9798)
/gene="Cgl0663"
                                                                                                                                                                                                                                                        complement (9094. .9798)
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(rrans] table=11
/product="Transcriptional regulators"
/product="A="BAB98055.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (7129. .8172)
/gene="Cgl0661"
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TAVSYMGTKDSEYFTTDSEHIRKVCHTLLAQLPMVLAMDIRRKKGLDIIAPDSSKSVA
ENLLSMVFGTGPESPASNEADVRDFEKSLLIYAEHSFNASTFTARVITSFKSDVYSAL
TGAIGALKGPLHGGANEFVMHTMLAIDDPNKAAAMINNALDNKNVVMGFGHRVYKRGD
                             /transi_table=11
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/protein_ide="BAB98056.1"
/db_xref="GI:21323429"
                                                                                                                                                                                                                                                                                  KSILTALINADSTGSQGIDIRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
/product="Malate/L-lactate dehydrogenases"
/protein_id="BAB98054.1"
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/protein_id="BAB98053.1"
/db_xref="GI:21323426"
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/EC_number="1.1.1.82"
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translation="MRFSRVLPALLITTAVSIPTASAATLTADTDKELCIASNTDDSA
                                                                                                                                       codon_start=1
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db_xref="GI:21323428"
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db_xref="GI:21323425"
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Query Match
Best Local Similarity
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       CGGGCTCGAAGCAAGGCCAAATGCGATGAATCGGTAATTACTGGAGAAAGGCACCGTGGAG
                                                                                                                               TCTTGGAATGAAACTCCCCAATATGACAACCTCAATCAAGGCTATGCAGAGACCTTGGAG
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/protesin_id="BAB99057.1"
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YDIPELPDNATIDEEKDILARYNAVKGSAVNPVLREGNSDRRAPIAVKNFVKKFPHRM
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GLAMLLPDDPTLADPNAEESFKTEYTYDEAKDIISGFSSDPASDVLSQLQQAATTGTR
TAEIRAEVFADRTDDYNESQTALKEDFQNCIDAIDDARPIPLQYILIGGAIALAVIVL
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NADP-dependent"
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                                                      GAGGGCCCCCGGCCATCCTCTCCGCGACACCCACCCCCGCGGAAATCATAGAGCGA
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CORDETVALIVE 0; MISRACE CGAGCGGGAGTCGGTGATCGGCCACTCT	JOURNAL Patent: EP 1108790-A 7061 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP) FEATURES Location/Qualifiers 1. 349980 /organism="Corynebacterium glutamicum" /mol type="genomic DNA" /db xref="texon:1718" /noTe="Seq 1 to long (3.309.400) split in 11, seq 7061 0.600.001 0.949.980 '" BASE COUNT 79274 a 90638 c 98727 g 81341 t Query Match 99.4%; Score 2111; DB 6; Length 349980; Best Local Similarity 100.0%; Pred. No. 0:		Db 211631 GTGGCCGGAACCCTCAGGGCCGTAAGCACCTCTGGCGGAATGGTCAACGACGTCC 2100	1861 ACCGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCCAACGCCTCTCCGAATTGGAT
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Tilg,Y., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel.
Process for the preparation of L-amino acids by ferme
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                                                                                                                                                                                                                                                            GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG
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        GGGGGCCCGCCGTGCTGATTGGGCAGGATCGCCGCTTCACGCTTGGGCCGCAGGAG
                             CTTTCTGGTGCGCGTGCGCGCATTGAGCCCGGCGTGCGCGTTGCCCCTGGCGCGCATC
                                        CTTTCTGGTGCGCGTGCTGGCGCATTGAGCCCCGGCTGTGCGCGTTGCCCTGGCGCGCATC
                                                                          GACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAG
                                                                                       GACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAAACGTTGGGGGCAGACGTCGTCAAG
                                                                                                                      TTTTCTCCAACAACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGT
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Db 1 GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC 60	; Conservative 0; Mismatches 0; In	cch 69.4%; al Similarity 100.0%;	/mol_type="genomic DNA" /db_xref="taxon:1718" BASE COUNT 275 a 414 c 456 g 328 t ORIGIN	KYOWA HAKKK Lc :e 1.	AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A. TITLE Novel polynucleotides JOURNAL Patent: EP 1108790-A 929 20-JUN-2001:	1 Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobact Corynebacterineae; Corynebacteriace; 1		RESULT 8 AX121013 AX121013 AX121013 DEFINITION Sequence 929 from Patent EP1108790.						1141 ATTGGTCAGGGGTTGGCGGTGGCGCGTGGCCAGGGGGGGCGATCTGGTCTACGCG 1708 GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGGGCGCTCGGCCATCCTCTTCCGC	1081 TCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCCGCCCGC	1021 ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGCTGAGGAGCTCGGCATTCCCAAGC	Db 961 CTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGGGGGGGG	Db 901 GGGGCCCGGCGTGGTGCTGATTGGCCAGGAGCTAAACCTGCCGAGCAGCACC 1527 Qy 1468 CTGCGTTTGCGCGTGGCATTTCGCTGGCGCGAGCTAAACCTGCCGATCGTGTCC 1527
Db 1081 TCGATTGCGCGCACCTTGTCCAÄGCTTATCGACGCTCCCCCACCGTTTCGGTCATT 1140 Qy 1648 ATTGGTCAGGGCGTTGGCGGTGGCGCGCTGGCCATGCTGGCCGATCTGGTCTACGCG 1707	1588 TCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCCCCC	Oy 1528 ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGCTCGGCATCGCAAGC 1587	Qy 1468 CTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGCGCGAGCTAAACCTGCCGATCGTGTCC 1527	Qy 1408 GGGGCCGGCCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGCTTGGGCCGCAGGAG 1467	Qy 1348 CTITCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCTGGCGCGCATC 1407	Qy 1288 GACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAG 1347	Qy 1228 TTTTCTCCAACAACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCGGCGTTCTCGT 1287	Qy 1168 TTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGT 1227	Qy 1108 CAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATT	Qy 1048 GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG 1107	Qy 988 GCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCAGATA 1047	Qy 928 CGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGC 987	Qy 868 CGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAG 927	Qy 808 ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCG 867	Qy 748 GATITITCCTTCCTCGGCGGTTCTTTGGGCACGGTCGGTGCGCATCATGAAGGCG 807	QY 688 GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCC 747	OY 628 AACCTCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGGCCAAATGCGAT 687	Qy 568 ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGAC 627

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REFERENCE
AUTHORS
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Replicable DNA, amino acid sequence, Corynebacterium micro
shuttle vector, and process for producing L-amino acid
Patent: JP 2001008693-A 2 16-JAN-2001;
DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMEH
OS Corynebacterium glutamicum
PN JP 2001008693-A/2
PD 16-JAN-2001
PF 24-MAY-2000 JP 2000153547
PF 27-MAY-1999 DE 19924365.4
PI IVERNE TILKE, LOTHAR EGGERING, BERNHARD EICKMANS, HERMAN
PI VETTYNA MECKEL
PC CLENIS/09, C12N1/21, C12P13/04, C12P13/06, C12P13/06, C12P
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°C C12P13/12,C12P13/20,C12P21/02//(C12N15/09,C12R1:15),(C12N1/21,
°C C12R1:15),
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27-MAY-1999 DE 19924365.4
IVENNE TILKE,LOTHAR EGGERING,BERNHARD EICKMANS,HERMANN ZAMU,
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:1718"
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E Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Vokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A. Novel polynucleotide

L Patent: JP 2002191370-A 929 09-JUL-2002;

KYOWA HAKKO KOGYO CO LTD

OS COrynebacterium glutamicum
PN JP 2002191370-A/929

PD 09-JUL-2002

PF 15-DEC-2000 JP 2000405096
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
PI KEIKO OCHIAI,
PI HARUHKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
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KYOWA HAKKO
OS COLYNNE
PN JP 200;
PN JP 200;
PN JP 200;
PI SATOSHI
PI KEIKO
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              /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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FEATURES	TITLE JOURNAL COMMENT	AUTHORS TITLE JOURNAL REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 11 AP005217/c LOCUS DEFINITION	Qy 1888 Db 1381 Qy 1948 Db 1441	Db 1261 Qy 1828 Db 1321		Db 1021 Qy 1588 Db 1081
Ibaraki, 305-8566 Japan Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan Itoh, T. is at the Japan Biological Information Research Center, Koto-ku, Tokyo, 135-0064 Japan Yamagishi, A. is at Tokyo University of Pharmacy and Life Science, Hachioji, Tokyo, 192-0392 Japan Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co., Inc., Kawasaki, Kanagawa, 210-861 Japan The other authors are at the National Institute of Technology and Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan.	Jurect Submission Submitted (17-MAY-2002) Director-General of Biotechnology Center, Wational Institute of Technology and Evaluation, Biotechnology Jenter; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan Jenter; Nishihara 2-49-10, Faillally Jenter, Jenter; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan Jenter; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-006	Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H., Nakamura,Y., Ikeo,K., Suzuki,M., Mashima,J., Itoh,T., Yamagishi,A., Nishio,Y., Usuda,Y. and Sugimoto,S. The entire genomic sequence of Corynebacterium efficiens YS-314 Published Only in Database (2002) 2 (bases 1 to 300750) Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H. and Director-General of Biotechnology Center.	AP005217 BA000035 AP005217.1 GI:23492722 AP005217.1 GI:23492722 Corynebacterium efficiens YS-314 Corynebacterium efficiens YS-314 Corynebacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.	APO05217 300750 bp DNA linear BCT 20-DEC-2002	GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGGGGGGACGCGAC 1947		ATTGGTCAGGGGGTTGGGGGTGGGGGCGTGGCCATGCTGGCCGATCTGGTCTACGGGGTGGTGAGGGGGTTGGGGGGTGGCGATGCTGGCCGATCTGGTCTACGGGGTGGTCAGGGGGTTGGGCGATGTGGGGGGGG	ATCATCGACACCT COGCGCGAATIST CGACGGCTGAGAGCICGCAATICGCAACCTGCAACCTGCAATIST CGACACCTGCAATIST CGACACCTGCAATIST CGACGGCGCGGCAGCGCAAGCTGAGCAGCTGAGGAGCTCGCCAAGCTTCGCAAGCTTATCGACGCTCCCCCCCC
CDS	gene	CDS		rrna CDS	gene	rRNA CDS	gene	cds
/note="CERNA03" 59257088 /note="CE0889, similar to AX063829-1 CAC25156.1 percent identity: 79 in 387 aa" /codon_start=1 /cadnsi_table=11 /product="putative aminotransferase" /protein_id="BAC17699.1" /db_xref="GI:23492727" /db_xref="GI:23492727" /ranslation="WRNKYVYERLRPFGETIFATMTORANEAGAINLGQGFPDEDGPA /translation="WRNKYYVERLRPFGETIFATMTORANEAGAINLGQGFPDEDGPA /translation="WRNKYYVERLRPFGETIFATMTORANEAGAINLGGGTPATMTORANEAGAINLGGTPATMTORANEAGAINLGGTPATMTORANEAGAINLGGTPATMTORANEAGAINLGGTPATMTORANEAGAINLGG	/translation="MRQQGSRYAIRAGRNLPDKEFRYLRMVIVTTAVYWGLNSQLRRL TQLTGPLNLPAPGRRQSVYINL" 56065725 /gene="rrnA_58" /gene="rrnA_58" /gene="rrnA_58" /gene="rrnA_58" /product="58_rnBosomal_RNA"	GRLT" GRLT" (a)4, .4594) /note="CE0888" /codon start=1 /transI_table=11 /product="hypothetical protein" /protein_id="BAC17698.1" /db_xref="GI:23492726"	/COGOD SCATT=1 /codon scart=1 /transI_table=11 /product="hypothetical protein" /protein_id="BAC17697.1" /db_xref="GI:23492725" /db_xref="GI:23492725" /transIation="MQAPILIPXLRCHFAEFLNHSSPERLSILYLTTCVGLGYGPNMHI /translation="MQAPILIPXLRCHFAEFLNHSSPERLSILYLTTCVGLGYGPNMHI /translation="MQAPILIPXLRCHFAEFLNHSSPERLSILYLTTPQSTKMLMLPHCVTPSLSY ARGFSRQYRITEFTDLRATHASNIMRYGFTNTSFHTLTPQSTKMLMLPHCVTPSLSY YOIRSHARHHHGDPEGRHVLIMVVSITDSPMARTLGYGNINPLSIDYACRPBLRFRLTLT YOIRSHARHHGDPEGRHVLIMVVSITDSPMARTLGYGNINPLSIDYACRPBLRFRLTLT	/gene="rrnA_238" 23995481 23995481 /gene="rrnA_238" /product="23s ribosomal RNA" /note="CErRNA02" complement(38084302)	/transI_table=11 /product="hypothetical protein" /protein_id="paC17696.1" /db_xref="G1:23492724" /translation="MSSQTPNSMPPTYHHHLGDVFADPWVMIHPITTCWWQPHPGSNT_NNPPHEHSPWWYY" 23995481	1936 "rrnA ct="1 "CETR "CEOR	/transl table=11 /transl table=11 /transl table=11 /product="hypothetical protein" /protein_id="BAC17695.1" /db_xref="G1:33492733" /db_xref="G1:33492733" /translation="MDQAPSGCLVDCVHGYIFYDTPVPMLLFPVGTSGNRKIVLDLFN /translation="MDQAPSGCLFGWVIGLFTPWHTHVYVCVVFCGEFDPGSGRTLAAC HYFWLNKPDRLITPLWSGCGCLFGWVIGLFTPWHTHVYVCVVFCGEFDPGSGRTLAAC LTHASRTMKFCLGGGLVANG" 5291936 /can=="rynalife"	1300750 /organiam="Corynebacterium efficiens YS-314" /mol_type="genomic DNA" /strain="YS-314" /db_xref="taxon:196164" 252620 /note="CE0885"

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Complement(12229. .12822)

/note="CE0894, similar to AX133781-1|CAC38957.1| percent

/Aentity: 71 in 195 aa"
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EVARLORMLIDALSTARASTLKEĞALGVRMVTRLTRELQVDEQQVARVVSLGVŞSĞLL
RRĞVPDPLPADDDĞĞDYIAPTEVADEMLQATIKAĞLAHIMRÇMYTQTYAAWLYŞEADE
KNKPHILLSPAŞRRDALPETRAMILQSLTRVĞEEDLEADLFFHHPLAASKI PRETIRH
LLEEARWIĞAVAĞĞĞVTSPARVLTQAPAĞVI PELADIAVAVRAPKÇVDYFIVQADYTV
WPGPLQPEMQKI IĞQLADLSSPĞLASVYRISEASLKHAMDLĞLTATEIEDFLTQHŞA
TĞLPĞYAYLLQDI ARRHĞTLRĞĞPALCYLRSDDPALLHŞAVEAĞALĞLÇAQIAPTVA
VSNAŞLI EVITALRKAĞMQPVAEDALĞASLDLAFRPARVPAARĞPAĞALĞLEĞIRIRA
AVAAIRREEVARTĞTVSDQPTLAVLQAAVRĞQKTVTLĞFVDXÇĞVAYHRTVKFĞTVNA
AVAAIRREEVARTĞTVSDQPTLAVLQAAVRĞQKTVTLĞFVDXÇĞVAYHRTVKFĞTVNA
GÇVDALDESTĞAVHREMLHRI TEVIVD"
                                                       /transl +=-
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GREGDVPSLIGPKRYDAFWKDLEAQGFIATADCVEVRTTWTDAERMVYATAETADRYR
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COMPLEMENT (9548. 11851)
/note="CE0892, similar to AE006976-11|AAK45126.1| percent
identity: 36 in 741 aa"
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qlsgiirnrpdtalplepglgslaarlorasiqravhtlsalelavleaaraqael
npitapevyerlhrälensaavptsacojgealmklrqllalvpggerfiilpetyatle
TNWQLLPEEHGRSLTFGEASQSIEALPARHRKILVTLYTSNGLGLTRDAALSADPARP
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/protein_id="BAC17700.1"
/db/ref="g1:23492728"
/tamblation="wfHPSFDVDEAYARKUNEFLRDTKRLQISAFFFGLVLLAIGGVL
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DVVLLALVNTNVDETLPPRWGLAVRTINRLGVHDRKLGERVPSVAVSGRRTIRDQDHW
DEISPWPITWGTDADVVRRAEKTIPHDLWNKLEKNRNRLDEVKNTRNMLLVL"
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ASLPGMWDRT I TVSSAAKTENVTGWKTGWALABAPI LIBAV I RAKIÇMS YVGAT PFQDA
VAHAVAHEKPWVKQMKKGLQNKRD I LTDALTQAGLKVHDSHGTYFVVADI GERJGGAEF
CFDL I DRVGVAA I PVQAFVDKPEQWSSKVRFAFCKQEDTLREAAQRLRAAGSI."
                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein"
/protein_id="BAC17703.1"
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/protein_id="BAC17702.1"
/db_xref="GI:23492730"
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identity: 75 in 547 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="CE0893, similar to AL583924-91|CAC31110.1| percent
|dentity: 50 in 62 aa"
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product="conserved hypothetical protein"
protein_id="BAC17704.1"
                                                                                                                                                                                                                                                                                                   translation="MGNMANVEKKGYVDPAWPDHDPSEGHVVTELIAPYAGAS:SPWGD
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transl_table=11
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Query Match
Best Local Similarity
Matches 1046; Conserv
25338 GAAACCACGTGGTGCGTGGGAGTCGATCATGATCACCCGGGAACCCCGGTCGCCCCGGGGT 25279
                                                    CGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTGACCCCGCAGAGGCCTGGAAT 1307
                                                                                                                                                                                                          GAAAACTGGTGTATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAAA 1187
                                                                                                        GATCATGAGGGTGTTGGGGGAGGCGTCGCCAGGCACGCCCCGTGAGCTCGCCGCACCCGG
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/protein id="BAC17705.1"
/db_xref="GI:23492733"
/translation="MAPGTVKMYDPERGFGFVSNPGGEDCFVGKQVLPKGVTELHQGQ
RIEFDFAAGRKGPQALRVKVLETPRRRPQHTYKPEELNGIISDMVTMLEGTVQPALLK
GHYPPRKVGEQVAKILRAVAKELEA"
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DRLANCESGGNWAINTGNGYHGGLQFSPSTWRAYGGDEFAPFAYQATREQQIAVAERT
LAGQGWGAWFACSSKLGLNSAPTPRNLNPAPAPAPAPAPAAYATVDTNTNPVVGSS
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Pred. No. 1.9e-146;
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Sahm,H.
Nucleotide sequence,
Corynebacterium glut
                                                       X66112.1 GI:505580

citrate synthase; glt gene.
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 3013)
                                                                                                                                                      C.glutamicum glt
X66112
                                             Eikmanns, B.J.,
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                   and transcriptional analysis
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Direct Submission
Submitted (15-MAY-1992) B.
Forschungszentrum Juelich
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2 (bases 1 to 3013)
TCCGAATTGGATAACAATCCGGAGAGGGCGGGACGCGACAGTCGCTTCACACGATTTGAG
                                                                                              ATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCAACGCCCTC
                                                                                                                                                                                                                                                                                    GGCGCGCTGGCCATGCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCC
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                                                                     ATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCAACGCCCTC
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838. .2151
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etglitedegyvstgsteskityidgdagilryrgvdiadlaematexesyllinge
lptpdelhkfndeirhtlldedfksgenvfprdahfmatlassvnilstyydddia
ldpadldkatvrlmakvpmlaayahrarkgapymydnnslanaemplampgyptepy
eidpimvkaldkllihadheoncststvrmigsaqanmfvsiagginalsgflhgga
noavlemlediksnhggdatefmnkvknkedgvrlmgfghrvyknydpraaivketah
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FAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGNESRKLVPREER"
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/protein id="CAA46903.1"
/db_xref="GI:550548"
/db_xref="SWISS-PROT:P42458"
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/protein_id="CAA46902.1"
/db_xref="GI:505581"
/db_xref="SWISS-PROT:P42457"
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/strain="ATCC13032"
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/EC_number="4.1.3.7"
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GmbH, I B T, Postfach 1913, 5170 Juelich,
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Submitted (25-APR-2001) The Institute for Genomic Research,
Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, C. Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
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Mycobacterium tuberculosis CDC1551
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae, Mycobacteriaceae, Mycobacterium, Mycobacterium
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AE006979 AE000516
AE006979.1 GI:138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE006979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGACGACGTCCGCCGACCTTCATGCCTGGAATTC 2499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGACGACGTCCGCCGACCTTCATGCCTGGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAGACAGTGGGTGGCCGGAACCCTCAGGGCCGTAAGCAGCCTCTGGCGGAATGGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAGACAGTGGGTGGCCGGAACCCTCAGGGCCGTAAGCAGCCTCTGGCCGAATGGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTTAGCGCAGTAAAGAAAATTATGCGCTGATCAAATCGATGATGAACACCAGGGTACG 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTTTAGCGCAGTAAAGAAAATTATGCGCTGATCAAATCGATGATGAACACCAGGGTACG 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGAATTGGATAACAATCCGGAGAGGGGGGGGACGCGACAGTCGCTTCACACGATTTGAG 2654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 17910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 17910)
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SCPLTILTTSTEAIGLAGEL/TWRVPPLSLTNDAIELFVDRARRVRSDFAINADTAVT
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45. .1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="clinical strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mycobacterium tuberculosis CDC1551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .17910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:13880475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="taxon:83331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 bp [
                                                                                                                                                                                                                                                                                                                                                                                   by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA linear BCT 27-APR-2001
, section 65 of 280 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2123
                                                                                                                                                                                                                                                                                                                                                                                 putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2088
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Sg
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AQTLTVFGLHTPHSVFGDTEGLAERLTAAVLASLNSVLAEPIQDVLWTDAQSKPCIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEYGGHEAAAAWQAMVDEPIGHAIAGAVANDLLRGVIATDALIGTFARWHEPSLMQNI
CFLYHLVGGGTGVWHVPIGGMGSVTSALATAAARHGAEIVTGADVFALDPDGTVRYHS
DGSDGAEHLVRGRFYLVGVTFAVLASLLGEPVAALAFGAQVKVNMVVRRLPRLRDDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRALDMLFILHADHEQNCSTSTVRLVGSSRANLFTSISGGINALMGPLHGGANQAVLE
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complement (6062.
                                                                                                                                                                                                                                                                                                                                 complement(6062. .6325)
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                                                                                                                                                                                                                                                                                                                                                                                                      TTTLDLQRTLGMTGGN1FHGALSWPFADNDDPLDTPARQWGVATDHERIMLCGSGARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (4429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAMVPVSLRDTAVIDVFGQGPGNKIGTLMCSLATHLASPVERLSAIRASMRDGKAAIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGTRLRRIAGRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLLSAPVDGAALNITCSGTNEQITFGLTGCRRAVPALSILTDQLAHELELLVGVSEAG
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                                                                                                                                                                                                   transl
                                                                                                                                                                                                                                                  note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="MT0921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="MT0920"
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                                                                                                                                                                                             _table=1
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                                                                                                                                           8.1"
                                                                                                                                                                                                                                                  Glimmer2;
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                                                                                                                                                                                                                                                  putative"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                           LENSPLGGARLVLRLPGPS"

complement (9473. .10183)
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| Tltgta,fssehkdavkraatsfwpdmkivnnievtgoappgpasgpcadlosainav
| Tggfia,fgndgaslipadyeiinrvadklkacpdarvtingytdntgseginiplsao
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7426. .7578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7575. .8105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="OmpA family protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="MT0923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="MT0922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MDFVIQWSCYLLAFLGGSAVAWVVVTLSIKRASRDEGAAEAPSA
      14.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .7578
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   Score 312.6;
DB 1;
                                                                                                                                           regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein family HMM"
Length 17910;
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γ	Qy db	Qу	Db Q	Db	Q 5	\$ 8	Db Qy	מם	δ	₽ Q	Ωу	B 8	. Db	, p, o,	Db Qy	Db Qy	db Vy	g &	D Qy	Bes Mat
1574 TCGGCATCGCAAGCTCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCTCCCCA 1	1514 TGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCCAGGCGGCTGAGGAGC 1	1454 TTGGGCCGCAGGAGCTGCGTTTTGCGCGTGGCATTTCGCTGGCGCGCGC	1409 GGGCCGGCCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGC 1	TGTCAGGAACCGATCAAGGCGAAGCGGCGACCACGCTGCTGGCGCTGGCCCGCTTTG	11050 GGCCGGACCGGCCGTCAGGCAGCTACTGCGACACGGCGCCACCGACCG	1289 ACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGGCAGACGTCGTCAAGC	1232 CTCCAACACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTG	GGTGCTCATCGACGCTCCCGAACCGCTTCCGGCAC	1172 GTGCAGCGGTGGCAAAAACCCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTT	1112 AGGCGGAGAAITTGGTGAAAACTGGTGTGATTGATTGAATTGTGTCGCCACTCCAATTGC	1052 TCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGC	992 TGGCCTCGTGGGGTTCATCTGGGCATCTCACCTTTTGCGGAACCCGGGGCGCAGATAGGTT	932 ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA	0 2	812 ACCGCGCCACAGAGCTGAAACTCCCACTGCTGCTCCCCTGCTTCCGGTGGTGCGCGCA	752 TITCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTGCGCATCATGAAGGCGATTC	692 CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT	632 TCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCCAAGGCCAAATGCGATGAAT	572 ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC	Best Local Similarity 54.0%; Pred. No. 3e-60; Matches 717; Conservative 0; Mismatches 589; Indels 21; Gaps
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available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, grg, or trg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rogers, J., Rutter, S., Seger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
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Notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence Nature 393 (6685), 537-544 (1998)
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Mycobacterium tuberculosis H37Rv
Bacteria; Actinobacteria, Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill,J
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1 (bases 1 to 37630)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jun 27, 1998 this sequence version replaced gi:1314009
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/translation="MAPTPGRRTRNGSVNGHPGMANYPDDANYRRSRRPPPMPSANR YLPPLGEQPEPERSRVPPRTTRAGERITVTRAAAMRSREMGSRWYLIVHRAATADGAD KSGLTALTMEPWANHAVDSAMAVALANTLFFAAAAGSESKRVALYLLITIAPFAVJA PLIGPALDRLOHGRRVALLALSFGLRTALLAVVLIMNYDGATGSPSWVLYPCALAMMVFS KSFSVLRSAVTPRVMPPTIDLVRVNSRLTVFGLLGGTIAGGAIAAGVEFVCTHLFQLP KSFSVLRSAVTPRVMPPTIDLVRVNSRLTVFGLLGGTIAGGAIAAGVEFVCTHLFQLP
                                                                                                                                                                                                                                                                                                                                                                          /note="Rv0876C, (MTCY31.04c), len: 548; unknown; possible membrane protein, highly similar to MTCB57 12 MYCD5712 MYCD5712 033057 HYPOTHETICAL 61.7 KI PROTEIN (579aa). FASTA scores: opt: 2850 z-score: 2863.4 E(): 0; 81.0% identity in 568 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transT_table=11
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ANTTSTLFREDTRLAVTIPTVDPQRGRLTGIVVQLLTLVVDHSGELRDVPHAEWSVRL
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VRTGSGALITGYRFDRTARDLHLLLPDPYTFPSNLLLTGAAPTVTGGTAVVGGVVSGGR
RRGDTRLFRHHDVLTGSVVGVRLPGMRGVPVVSGCRRFIGYPYIVTGAADISTTGS
RRFDTRLFRHHDVLTGGLSPDERALVSHGLQIGIVVDEHLAAPGQGDFVIRGLLGADESTGS
IEIDEVQUGATMGFQVRDAAGADKDLRLTVERAAARLPGRAAGALLFTCNGRGRRMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Rv0876c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Rv0876c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Rv0875c, (MTCV31.03c), len: 162, unknown, possibly exported protein, highly similar toMLCB57_II Mycobacterium leprae cosmid B57, 033056 HYPOTHETICAL 18.1 KD PROTEIN (162aa). FASTA scores: opt: 789 z-score: 963.4 E(): 0;
                                                                                                                                                                        /producT="hypothetical protein Rv0876c"
/protein id="CAA97383.1"
/db_xref="GI:1314013"
/db_xref="SWISS-PROT:Q10564"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Rv0875c"
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NFAGNETSARLÓLGRPAVLVVRCTVLVTVLAIAAXPGSLAATALATLITAGSSAIAK
ASLDASLOHDLPEESRASGFGRSESTLQLAWVLGGAVGVLVYTELWVGFTAVSALLIL
GLAQTIVSFRGDSLIPGLGGNRFVMAEQETTRRGAAVAPQ"
complement (3457. . 3465)
                       /gene="Rv0880"
6442. .6873
                                                                          /db_xref="SWISS.-PROT:Q10541"
/translation="MSVENSQIREPPPLEPVLLEVWPVIAVGALAWLVAAVAAFVVPG
LASWRPVTVAGLATGLLGTTIFVWQLAAARRGARGAQAGLETYLDPK"
                                                                                                                                                                                                                                                                                                                        /gene="Rv0879c"
complement (5989. .6264)
                                                                                                                                                                                                                                                                                                                                                             /note="gga (or aagg) po
complement(5989. .6264)
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complement (5719. .5721)
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fslliggltagegsamgepaaaamaaaaaptlswilmaatrareghaaggraaaaytea
araatahealvaanraugllsvilsbilegonleaplatateasyeolwapdyaamveyaga
araatahealvaanraugllsvilpevutaapaagavgvpaalaipalgvenigvgneligignig
navvasqltpmqollsvilpevutaapaagavgvpaalaipalgvenigvgnoentnergga
navvasgentgdxnefgicnignanligngnignanliggranaptraggllntgigspvtogran
agelnigsgenegsgilegnapdnigngssgegnaabdtssgenagtaltrasstwa
sgegntgtghgefensgnsgsgeponlgngssgegnaabdtssgeponagtaltrasstwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Rv0878c, (MTCY31.06c), len: 443, unknown; similar to YHS6 MYCTU P42611 hypothetical 50.6 kd protein in hsp65 3' region, (517 aa), FASTA scores: opt: 1044, z-score: 954.9, E(): 0, (47.4% identity in 397 aa overlap). Similar also to MTV014 3; MTC165 2, MTCY98 24, MTCY3C7 23, MTCY48 17, MTV004 5, MTV004 3 etc."
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                                                                                                                                  /codon_start=1
/trans1_table=11
/product="hypothetical protein Rv0879c"
/protein_id="CAA97386.1"
/db_xref="GI:1314017"
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complement(4380.
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/note="Rv0877,
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3583. .4371
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/note="Rv0879c, (MTCY31.07c), len: 91 unknown, equivalent
/note="Rv0879c, (MTCY31.07c), len: 91 unknown, equivalent
to MLCB57 14 Mycobacterium leprae O33059 HYPOTHETICAL 9.8
KD PROTEIN (91 aa), E(): 1.2e-25, 76.9% identity in 91 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="PPE"
/protein_id="CAA97385.1"
/db_xref="GI:1314016"
/db_xref="SWISS-PROT:Q10540"
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/protein_id="CAA97384.1"
/db_xref="SWISS-PROT:Q10539"
/db_xref="SWISS-PROT:Q10539"
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3583. .4371
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Similarity
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                                                        GGGCCGGCCCGTGGTGCTGATTGGGCAG----
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                                                                                                                                                                                                                                                                                      Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex 15, France e-mailtgarnier@pasteur fr Submitted on behalf of the Mycobacterium bovis sequencing teams, TB Research Group, Veterinary Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestorie, Survey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK. PT4 Annotation, Genopole, Institut Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France. Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCCGCTGGTGCTGGTCATTGACGCGGCCGGACCCGCGTTGTCGGCCGCAGCCGAACAGG 34641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGC 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGGCCCGCTGCGTTACGCGAAGCCCGACGCGGGATGGCGCTCGCCGCCGAGCTGTGCC 34701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence of Mycobacterium
                                                                            /mol_type="genomic DNA"
/strain="AF2122/97"
                                                                                                                                                            organism="Mycobacterium bovis subsp. bovis AF2122/97"
                                                                                                                                                                                                                                                      ocation/Qualifiers
                                        xref="taxon:233413"
                                                                                                                                                                                                                  327650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34461
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len: 373 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 373 aa overlap). Probable citA (alternate gene name: gltA), citrate synthase 2 (EC 4.1.3.7), highly similar to others e.g.
CAB95899.1|AL359988 putative citrate synthase from Streptomyces coelicolor (387 aa); P39119|CISY_BACSU citrate synthase II from Bacillus subtilis (366 aa), FASTA scores: opt: 586, E(): 5.8e-30, (33.8% identity in 367 aa overlap); etc. Also similar to Rv0996|MTCY31.24 from Mycobacterium tuberculosis (29.2% identity in 274 aa overlap) and Rv1131. Contains PS00480 Citrate synthase signature. BELONGS TO THE CITRATE SYNTHASE FAMILY."
(99.9% identity in 882 as overlap). Probable transcriptional regulatory protein, LuxR family, highly similar (but shorter 238 as in N-terminus) to NP_30220.1|NC_002677 possible transcriptional regulator from Mycobacterium leprae (1106 as). Also highly similar (generally in part) to otherse e.g. T50568 probable multi-domain regulatory procein from Streptomyces coelicolor (1334 as); P10957|NARL ECOLOR (216 as), PASTA scores opt: 193, E(): 6e-06, (37.4% identity in 99 as overlap); etc. Also highly similar to others from an overlap); etc. Also highly similar to others from the control of the coefficient of the coeffic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="Mb0914c"
complement(3413. .6061)
/locus_tag="Mb0914c"
/note="Mb0914c, -, len: 882 aa. Equivalent to Rv0890c,
len: 882 aa, from Mycobacterium tuberculosis strain H37Rv,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHIEAIDAYWVSAAEHGMNASTFTARVIASTGADVAAALSGAIGAMSGPLHGGAPARV
LPMLDEVERAGDARSVVKGILDRGEKLMGFGHRVYRAEDPRARVLRAAAERLGAPRYE
VAVAVEQAALSELREERPDRAIETNVEFWAAVVLDFARVPANMPAMFTCGRTAGWCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="PROBABLE CITRATE SYNTHASE II CITA"
/protein id="CAD93774.1"
/db_xref="GI:31617665"
/translation="WIVDENSFVPGLDGVVAFTTEIAEPDKDGGALRYRGVDIEDLVS
ORVTFGDVWALLVDGNFGSGLPPAEPFPLPIHSGDVRVDVQAGLAMLAPIWGYAPLLD
IDDATARQOLARASYWALSYVAQSARGIYQPAVPQRIIDECSTVTARFWTRWCGEPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HILEQKRLGKLVRPSAIYVGPGPRSPESVDGWERVLTTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTIGGDFSMLTYNIAGLPFPLSSAILPRFYYTKEIGKKLNAYYVANVQEDFAYHQFLI
KKSKMPSQTPPEPPTLHWPIGVPFSDGLHTLSSFKYQBLLDRQTWTECTSDNCLTLLKGF
TYSQMRLPGGDTVDVYNLHTMTGGPFAPTTMANLAQVANYIQQNSAGRAVITYGDFPARP
SDDQSALLQFAQVNGLTDAMVQVEHGPTTPPFAPTCMVGNECELLDKIFYRSGQGVTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="Mb0913c"
complement(2205. .3326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAVSYGNEAPKFFNSKGEPLSDHSPAVVGFHYVADNVAVR"
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ENRTPVANPQQVSVPEGGTVGPVRFDACDPDGNRWTFAVRERGAPGGPQHGI VTVDQR
TASFI YTADPGFVGTDTFSVNVSDDTSLHVHGLAGYLGPFHGHDDVATVTVFVGNTPT
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transl_table=11
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/protein_id="CAD93773.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="Mb0912'
698. .2170
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EC_number="2.3.3.1"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="citA"
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/note="Mb0915C, ", len: 285 aa. Equivalent to Rv0891C, len: 285 aa, from Mycobacterium tuberculosis strain H37Rv, (99.6% identity in 285 aa overlap); Possible transcriptional regulator, highly similar in N-terminus to NP_302202.1 |NC_002677 possible transcriptional regulator from Mycobacterium leprae (1106 aa). Also highly similar to several Mycobacterium tuberculosis putative transcriptional regulators e.g. Q1102 |MTCY02B10 22 PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN (1159 aa), PASTA Scores: opt: 702, E(): 8.3e-40, (50.6% identity in 247 aa overlap); MTV036 21; MTV008 44; MTCY02B10 23 shows similarity with several adenylate cyclases and hydrolases from other organisms."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAANGE LITTURE TO MOET IN NEW SONS I DEAVE LE ALKASK VURGETIANH
NAANGE ICRELIGIE PLAIE FRAARV KRIS FLEIA DELDE HE ALKASK VURGET LANH
NAANGE ICRELIGIE PLAIE FRAARV KRIS FLEIA DELDE HE HELKEGGVEGA VURQOT
LRAS I DWSHALLTETEQI LERRLAP FVGGED LAAVRAVAAGS DLDEFS VLDOLTILVD
KSLVVADDC GCRTRYRLLETVERYALEKIGDS GEADVHAHR DYYTALAA SLINTPADN
HORLUVARAFETE I DUILRAA FAWSRENGHI TEALQILAS SLOP I WEGRAHLREGLSWENS
I LEDOR FHRLAVSTAVRARALADKAMIS TWLATS PVGATDI I AFAQQALAMAREVOD
AALVRALTACGCS SCYNABEAAAP YFARATDLARA I DDKWTLCQI LYWRGVGTCI SGDP
NALRAAAEECRD LADTIGDR FVSRHCSLWLSILAQMWAGNLTEALELSER I TAEAEBASN
DVPTKVLGLYTOAQVILAY CGASAAHAI AGACI AAATELGGVYQGI GYAAMTYAALAAG
DVPTKVLGLYTOAQVILAY CGASAAHAI AGACI AAATELGGVYQGI GYAAMTYAALAAG
DVTAALEAS DAAR PILRAQ PDQVTMHQVLMAQLALAGGDA I AAROFANDAVDATNGWH
RWVALT I RARVATARGSFELASDDAHAAIACGAELHI Y CGMPDAMELLAGLAGEVGSH
SEGVRLLAGAAAAROQTROVERKIWDAGYQASVTALREAMGDED FDRAWAEGAALSTD
EAIAY AQRGRERKREARGWGS ITPTEEDVVRLVSEGLSNKDI AKRLEVSPRTVQTHL
THVYAKLGLASR VQLVDEAARRGSPS"
         CAB59668.1 AL132674 monocxygenase from Streptomyces coelicolor (519 aa), P12015 CYMO ACIS cyclohexanone monocxygenase from Acinetobacter sp. (542 aa), PASTA scores: opt: 489, E(): 6.8e-26, (30.3% identity in 492 aa overlap); etc. Also highly similar to Rv0565c, Rv3854c,
                                                                                                                                                                                                                                   /note="Mb0916, -, len: 495 aa. Equivalent to Rv0892, len: 495 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 495 aa overlap). Probable monooxygenase (EC 1.14.-.-), highly similar to others e.g NP_250787.1|NC_002516 probable flavin-binding monooxygenase from Pseudomonas aeruginosa (491 aa);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRLPADAWLVDLGRHPLRGLFRPEWVMQLCHPDIREKFPPLRTAKSSPTSILPAQFTT
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/db_xref="G1:31617667"

/db_xref="G1:31617667"

/translation="MLFNAVHNSLPENIDIDHAILRGEDHPPTCAKCVARGRISALGS

/translation="MLFNAVHNSLPENIDIDHAILRGEDHPPTCAKCVARGRISALGS

LDLRYHSLRCYAAPPDVGRCEEVPPRRRVLIANQGLDVSRLPPTGTVTLLLADVEEST

HLWQMCPEDMATAIAHLDHTVSEAITNHGGVQPVKRYEGDSFVAAFTRASDAAACALD

LQRTSIAPIRLRIGLHTGEVQLRDELYVGPTINRTARLRDLAHGGQVVLSAATGDLVT
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BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVGRRAQIS"
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ELLGACPELTILATSREPIGMAGEITWRVPSMSITDEAVELFADRASRVQPGFTIANH
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/transl_table=11
/product="pOSSIBLE_TRANSCRIPTIONAL_REGULATORY_PROTEIN"
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(probably LUXR-FAMILY)"
(protein id="CAD93775.1"
(db_xref="GI:31617666"
(translation="MEALLAQURLVTLCGTGGVGKTRLAIQIASASELRDGLCFVDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EC_number="1.14.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   locus_tag="Mb0916"
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etc
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                                                                                                                                                            CGCAGACGCCCGCGCCCGTACCCGATGTGCCCACGTGGGACTCGGTGGTGGCATCGCGCC
                                                                                                                                                                                                      CTCCAACAACTCCTGGCGTGGCA----CTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTG
                                                                                                                                                                                                                                                                                            GTGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTT 1231
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/product="PROBABLE_MONOOXYGENASE"
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Search completed: November 13, 2003, 00:10:28 Job time: 7983.97 secs

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Minimum DB
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					L-lysine; animal feed;						Genomic sequence o Listeria monocytog	DNA sequence upstr	2CFE 67 coding seq	otoc	Listeria innocua c	Streptococcus poly Streptococcus poly	Streptococcus pneu	Streptococcus pneu	S. pneumoniae deri	CFE 67 coding sequ	Bacillus clausii g S. pneumoniae type	Streptococcus pneu	DNA encoding novel	E. coli DNA for ce	Human R1128 gene c	N. meningitidis B	H. pylori GHPO 451	Helicobacter pylor	Helicobacter pylor	Enterococcus faeca		N. gonorrhoeae nuc	Pseudomonas aerugi	m codi	

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07-APR-2000;
03-AUG-2000;
The present invention provides a number of nucleotide and protein sequences from the Corymeform bacterium Corymebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of corymeform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Corymeform bacterium, and identifying a homologue of a gene derived from corymeform bacterium. Corymeform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO: 7061; 246pp + Sequence Listing; English.
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Senoh A, Ikeda M, Ozaki A;
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Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering; ds.
    Corynebacterium
                                                                                                                                                                                    Corynebacterium glutamicum MCT protein encoding
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Pompejus Z, Kroeger ß Schroeder Ή Zelder Ó Haberhauer G

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AAF68082 and AAF68082 represent sequencing primers which are used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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1808	CTCGGCCATCCTCTTCCGCGACACCCACCCACCGCCGGAAATCATAGAGCGACAAGGCGT:	1749	δ
1320		1261	В
1748	CGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGC :	1689	ş
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1688	ccccaccetttcggtcattattggtcagggcgttggcgtggcg	1629	γΩ
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1628	GGAGCTCGGCATCGCAAGCTCGATTGCGGCGCACCTTGTCCAAGCTTATCGACGCTCCCCT	1569	ş
1140	AAACCTGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGA	1081	ф
1568		1509	γQ
1080		1021	В
1508	CACGCTTGGGCCGCAGGAGCTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGCGCGC	1449	ş
1020	CGTTGCCCTGGCGCGCATCGGGGGCCCGCCTTGTTGGTGATTGGGCAGGATCGCCGCTT	961	ф
1448		1389	Ş
960		901	皮
1388	GGGGGCAGACGTCGTCAAGCTTTTCTGGTGCGCGTGCTGCCGCATTGAGCCCGGCTGTGCG	1329	ş
900	GCGATTGCGCGTTCTCGTGACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTT	841	g
1328		1269	Ş
840	GTAGAGGCAACGGATCGTTTTTCTCCAACAACTCCTGGCGTGGCACTTCCGGTGATGGA	781	皮
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780	AATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAAAAAACCCTCAAGGTTATTCAGCC	721	망
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                    Sequence 1473 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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508 GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC 567	Query Match 69.4%; Score 1473; DB 22; Length 1473; Best Local Similarity 100.0%; Pred. No. 0; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	userul in animal reeds, in human medicine and in the pharmaceutical industry. Sequence 1473 BP; 275 A; 414 C; 456 G; 328 T; 0 other;	(4) a process for producing L-amino acids, comprising culturing a coryneform bacterium that overexpresses the accDA gene. Coryneform bacteria transformed with (I) so that they overexpress the accDA gene are useful for producing L-amino acids, especially L-lysine, which are	The invention also describes (1) a polypeptide derived from (1) having a fully defined 491 aa sequence; (2) coryneform microorganisms transformed with one or more copies of (1); (3) the shuttle vector pZiaccDA contained in Corynebacterium glutamicum DSM 12785; and	Disclosure, Page 12-15, 20pp, German. This invention describes a novel cloned Corynebacterium glutamicum DNA (I), replicable in coryneform microorganisms coding for an accDA gene	Cloned Corynebacterium glutamicum accDA gene useful for producing transformed coryneform bacteria producing increased yields of L-amino acids, especially L-lysine	WPI; 2001-042411/06. P-PSDB; AAB45789.	(DEGS) DEGUSSA-HUELS AG. (KERJ) PORSCHUNGSZENTRUM JUELICH GMBH. Tilg Y, Eggeling L, Eikmanns B, Sahm H, Moeckel B;	10-MAY-2000; 2000EP-0109842. 27-MAY-1999; 99DE-1024365.	EP1055725-A2. 29-NOV-2000.	medicine; pharmaceuticai industry; ds. Corynebacterium glutamicum.	C. glutamicum accDA DNA #2. L-amino acid; accDA; coryneform microorganism; L-lysine; animal feed;	AAC82733; 15-MAR-2001 (first entry)	RESULT 5 AAC82733 ID AAC82733 standard; DNA; 1473 BP. XX	1948 AGTCGCTTCACACGATTTGAGCGTTTTAGCGCAG 1980
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Best Local Similarity
Matches 717; Conser
                                                                                                                                This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polymucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
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                                                                                                                                                     The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequence of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English
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                                                                             Note: The sequence data for this patent did not form specification, but was obtained in electronic format
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	Fleischmann RD, White OR, Fraser CM, Venter JC;	YPI
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                                   This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                              New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum -
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                                                                                                                                                                  Claim 1; Page 154; 709pp; German.
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Best Local S
Matches 168
                                                                                                                     The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                         in the exemplification of the invention.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000;
03-AUG-2000;
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                                                 European
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DB; AAG93188.
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                                                      Patent
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO: 3442;
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Conservative
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Senoh A,
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                                                                                                                                                                                                                                                                                                                                                                                                     246pp + Sequence Listing;
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Pred. No. 6.3e-41
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      The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in
                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                              New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                         Claim 27;
                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                        Haselbeck R,
Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibiotic;
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DB; AAU36304.
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2000US-206848P.

2000US-207727P.

; 2000US-242578P.

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; 2000US-257931P.
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Xu HH;
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Pred. No. 2.2e-29;
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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
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 13-FEB-2002
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                                                                                                                                                                                                                                           CC The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPD at
                                                                                                                                                                                Best Loc
Matches
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23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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22-DEC-2000;
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                                                                                      TCCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAG
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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antibacterial; drug design.
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Xu HH;
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               A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to
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06-MAY-1997;
16-MAY-1997;
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                                                                                 US2002120116-A1
                                                                                                              Enterococcus faecalis
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Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardner, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
12655398
Other GSS: AG-ND-133C23.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                   Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Anopheles gambiae
Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                       , genomic survey sequence.
BH379574
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BH987475 oej71e06.
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BH994577 oei62f03.
AW587803 ST67B11 P
BH925341 odi46f02.
BZ53368 pacs1-60
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AG247247 Lotus jap
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AI222631 EST226326
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BH988285 Oej67b06.
BZ012471 Oed23c11.
BZ033778 Oed01001.
BZ033778 Oed01010.
BZ017314 Oei67c12.
BH930860 Odj01b11.
BZ075724 lki53c01.
BZ075724 lki53c01.
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BZ033142 Oeh45a09.
BZ071328 lju13h07.
BH715901 BOHYJG4TF
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BH705901 BOHYJG4TF
BH705901 CAB40003
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BZ0052334 jnr68b12.
BH397912 AGG-ND-143
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RESULT 2
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VERSION
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This clone is from an A. gambiae BAC library (ND-TAM) provided by This clone is from A. gambiae PEST strain (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed genese of larvae. The BAC library was constructed at Texas A&M University BAC Center University. College Station, Texas 77843-2123, USA using a HindIII
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Seq primer: M13 For
Class: BAC ends.
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/mol_type="genomic DN
/strain="PEST"
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/86 c 109 g 156 t
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C. reinhardtii CC-1690 (mt+), CC-1691 (mt-), Gamete
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="C. reinhardtii CC-1690 (mt+), CC-1691 (mt-), Cdomete [hormalized], Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Gamete library was constructed by Hui Zhao, Min Lu, Jeffrey McDermott, William J. Snell and John Davies.
Strain 21gr cells (CC-1691; mating type plus) and strain 6145c cells(CC-1691; mating type minus) that had been growing on a light-dark cycle (13:11 L/D) in R-medium (Sager and Granick) were separately transferred into nitrogen-free medium at 8 hours into the light period. PolyA mRNA was purified from each sample every 2 hours for the next 18 hours. The mRNA was pooled and used for cDNA synthesis. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="21gr (CC-1690 wild type mt+) & 6145c (CC-1691 wild type mt-)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Michael A. Grusak
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 773)
Grusak, M.A., Samac, D.A.,
,J. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;
Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;
Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI311746 773 bp mRNA linear EST 20-JUL-2001
EST5313496 GESD Medicago truncatula cDNA clone pGESD15E20 5' end,
mRNA sequence.
BI311746
BI311746.1 GI:14986073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B398601e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mgrusak@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR sequence name: MTPAZ34TK
More information is available
seq primer: SKmod (CTA 9AA CTA
Location/Qualifiers
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/db xref="taxon:3880"
/clone="pGESD15E20"
/tissue_type="immature seeds"
/tissue_type="immature seeds, 11 to 19 days after
/dev stage="Immature seeds, 11 to 19 days after
/delone_type="Immature seeds, 11 to 19 days after
/clone_type="GESD"
/clone_type="GESD"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Display: pBluescript SK-; Site_1: Display: pBluescript SK-; D
                                                                                                                                                                                                                                                                                                                                              /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
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RESULT 5
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ORGANISM
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                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                   1063 bp DNA linear GSS 17-DEC pacs1-60_1377.s1 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60_1377, genomic survey sequence.
                  Whole-Genome-Sequence variation among Psedomonas aeruginosa library J. Bacteriol., (2002) In press
                                                                                                                                                                  Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                    Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                           Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1063)
                                                                                                       Spencer, D.H.,
                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                  BZ548722.1 GI:27152303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAGATAGGT 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATGCTACCAATCAACGTTTACCTCTTATTATAGTATGTGCGTCTGGAGGAGCGCGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGCTGAATTTTTATTCGAAAAGGGTGCATTTGATTCACTCGTACCAC 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICCIGGGICCICGCGIGGAGITAACCACIGGGCAIGCGCITCCAGACGGIGIGCAG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAGCTAGTTTTGGAATGTTGGGGGATATCATTCTTGCCGAACCCGATGCTTACATAGCA
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  Bacteriol.,
ntact: Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.9%;
48.6%;
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Raymond
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Pred. No. 1.7e-12;
0; Mismatches 269;
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                                                             multiple isolates
                                                                                                       Sims, E.E.,
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Ş 닭 8 뮍 S 멍 S 밁 Ś В δ 밁 Ş 밁 8 B Ś

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VERSION
KEYWORDS
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DEFINITION
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COMMENT
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ORIGIN
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            TITLE
JOURNAL
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Best Local Sim
Matches 206;
                                                                  AUTHORS
                                                                                                                                                                         ORGANISM
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University of Washington
Box 352145, Seattle, WA 99
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
            ESTs from developing 
Unpublished
                                                                Grusak, M.A.,
                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                      Medicago truncatula
                                                                                                                                                                                                                                                                             BI310727
712 bp mRNA linear EST 20-JUL-2001
EST5312477 GESD Medicago truncatula cDNA clone pGESD8J24 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: craymond@u.washington.edu Class: shotgun.
                                                                                                                                                                                        Medicago truncatula (barrel medic)
                                                                                                                                                                                                                             BI310727.1
                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGATGCCGATCCTCACCTTCATCGACACGCCCCGGCGCCTACCCGGGGATCGATGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCTGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGA 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACGCTTGGGCCGCAGGAGCTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGCGAGCT 1508
                                                                                                                                                                                                                                                                                                                                                                                          CACCGCCGAGCGCCTGAAAGGCCTGGGCATCGTCGACAAGGTCATCGACGAACC 471
                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAAC 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCGGCCATCCTCTTCCGCGACCAACCAACCGCGCGGAAATCATAGAGCGACAAGGCGT 1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAACGCGGCCAAAGCGAGGCGATCGCCTGGAACCTGCGGGTGATGGCGCGACTGAAGAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGCTCGGCATCGCAAGCTCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCT 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATGCCGCGTCCGGAAGGCTATCGCAAGGCCTGTCGCCTGATGGAAATGGCCGAACGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCTCCATCCTCTGGAAGACCGCCGAGAAGGCCGCCGAGGCCATGGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCGATCTGGTCTACGCGGCCGAAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGC 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCGACCAGTTGAACATGCTGCAATACTCCACCTATTCGGTGATCTCGCCGGAAGGATG
                                                                               (bases 1 to 712)
                                              sak,M.A., Samac,D.A.,
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="pacs1-60_1377"
/clone_lib="pacs1-60"
/note="clinical isolate 1-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Pseudomonas aeruginosa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%;
                                                                                                                                                                                                                             GI:14985054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                             reproductive tissues of Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 g
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Pred. No. 5.2e-12;
0; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98105-2145,
                                                                Town, C.D.,
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                                                              Aken, S., Utterback, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
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Michael A. Grusak

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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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                                             1051
      483
                                                                                        423
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                                                                                                                                                                                                                                                                   303
                                                                                                                                                                                                                                                                                                            874
                                                                                                                                                                                                                                                                                                                                                     243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694
                                                                                                                                                                                                                                                                                                                                                                                         814 CGCGCCACAGAGCTGAAACTCCCACTGCTGCTCCCCTGCTTCCGGTGGTGCGCGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                754 TCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634 AATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCCAAGGCCAAATGCGATGAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR sequence name: MTPAL60TK
More information is available at:
Seq primer: SKmod (CTA 9AA CTA 9t9
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1100 Bates Street, Houston, Tel: 713-798-7044 Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA/ARS Children's Nutrition Research Center
                                                                                                                                                                                                                                                                                                       CAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCAC
                                                                                                                                                                                                                 CGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAA---TCCCACGATGGGTGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCAAACAGGCACAGGTCAAGTAAATGGTATTCCTGTAGCAATAGGTATTATGGATTTT
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TTTGCAGGTAAAAGAGTAATTGAAGAAACGTTGAAGATCGAAGTGCCCGAAGGTATACAA
                                        TTCCTGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAG 111
                                                                                    ACAGCTAGTTTTGGAATGTTGGGGGATATCATTCTTGCCGAACCCGATGCTTACATAGCA
                                                                                                                             ATGGCCTCGTGGGGTTCATCTGGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGT 1050
                                                                                                                                                                          CAPATCAPAAAGTTATTCTATGTACCGATACTTACATCTCCTACTACTGGTGGGGGTA
                                                                                                                                                                                                                                                            CAAGAAGGAAGTTTGAGCTTAATGCAAATGGCTAAAATTTCTGCTTCTTTATATAATTAT
                                                                                                                                                                                                                                                                                                                                                TATGCTACCAATCAACGTTTACCTCTTATTATAGTATGTGCGTCTGGAGGAGCGCGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGATGATTATCAAAATCGTCTTGATTCTTATCAAGACAGAACTGGATTACTGGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA-enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="immature seeds"
/dev_stage="Immature seeds, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="pGESD8J24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type="mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immature seeds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lib="GESD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
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Best Local Similarity
Matches 235; Conserv
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USDA/ARS Children's Nutrition
Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grusak, M.A., Samac, D.A., T
Cheung, F. and Fraser, C.M.
More ESTs from developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR sequence name: MTPBX17TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA 9AA CTA gtg 9AT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100 Bates Street, Houston,
Tel: 713 798 7044
Fax: 713 798 7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Medicago truncatula (barrel medic)

Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mgrusak@bcm.tmc.edu
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GATTTTGAGTTATGGGAGGTAGTATGGGATCCGTAGTGGGTGAGAAAATCACTCGGTTG
                                      GATTTTTCCTTCCGCGGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCG 807
                                                                                 GATGCGGTTCAAACAGGCACAGGTCAAGTAAATGGTATTCCTGTAGCAATAGGTATTATG 61
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                                                                                                                                                                                                                                                                                    171
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                /notes Tvector: Biluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propogated in
XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Immature
pollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Medicago truncatula"
|mol_type="mRNA"
|oultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="GESD"
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49.5%;
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EST486683 MHAM Medicago truncatula/Glomus versiforme
library cDNA clone pMHAM-20E21 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Noble EST name: N380393e TIGR sequence name: MTDBW35TK information is available at: http://www.medicago.org Seq primer: SKmod (CTA 9AA CTA gtg gAT CC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glomus versiforme, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Samuel Roberts Noble Foundation
Sam Noble Parkway, Ardmore, OK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mjharrison@noble.org
/clone lib="MHAM"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript Sk-; Site_1: EcoRI; Site_2: EcoRI; Site_2:
/note="Vector: pBluescript Sk-; Site_1: EcoRI; Site_2: Eco
                                                                                                                                                                     /tissue_type="roots colonized with Glomus versiforme"
/dev gtage="Roots harvested at 10, 17, 22, 31 and 38 post-inoculation with Glomus versiforme. The library made from a mixture of RNA from each of these stages.
/lab.bost="E...coli strain XLOLR"
                                                                                                                                                                                                                                                                                                       'clone="pMHAM-20E21"
                                                                                                                                                                                                                                                                                                                                                  'mol_type="mRNA"
'cultivar="Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Medicago truncatula/Glomus versiforme
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pacs2-164 3167.y3 pacs2-164 Pseudomonas pacs2-164_3167, genomic survey sequence.
                                                                                                   BZ561247.1
GSS.
                                                   Pseudomonas aeruginosa
Pseudomonadaceae; Pseudomonas
                              Bacteria; Proteobacteria;
                                                                               Pseudomonas aeruginosa
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112 c 151 g 265 t
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J. Bacteriol., (:
Contact: Chris K.
                                                                                                                                            University of Washington Box 352145, Seattle, WA
                                                                                                                                                                                                                             Whole-Genome-Sequence variation among Psedomonas aeruginosa library
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Spencer,D.H., Raymond,C.K., Smith,E.E.,
Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                            Tel: 2062216954
                                                                                                                                                                                Genome Center
                                                                                                            2066857244
                                                                         shotgun
                                                                                      craymond@u.washington
                                                         Location/Qualifiers
/organism="Pseudomonas
/mol_type="genomic DNA"
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Eukaryota; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                          1031080C09.y1 (
Lambda Zap II (
BI725661
                                                                                               Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                              Unpublished
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                           Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulat: Vascular Plants. Project: 1031
                                                                                                                                                                                                                                                                                                                                                                                           BI725661.1 GI:15701356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                   chauser@duke.edu.
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
                                                   1. .539
                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="2-164"
/db xref="taxon:287"
/db yref="taxon:287"
/clone="pacs2-164"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library."
                                                                                                                                                                                                                                                                                                                                                                                                                  C. reinhardtıı
Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                               539 bp mRNA 111
reinhardtii CC-1690, Stress:
Lamydomonas reinhardtii cDNA,
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90, Stress II (normalized),
rdtii cDNA, mRNA sequence.
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REFERENCE
AUTHORS
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ACCESSION
VERSION
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AG247247
LOCUS
        REFERENCE
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                                                            TITLE
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Best Local Similarity
                                  JOURNAL
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                                                                                                                                Lotus japonicus Lotus japonicus Lotus japonicus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
Lotus japonicus TAC End sequences
Published Only in Database (2002)
2 (bases 1 to 652)
                                                                                                                                                                                                                                                                                                            AG247247.1
GSS.
                                                                                                                                                                                                                                                                                                                                                          Lotus japonicus
AG247247
                                                                                        Sato, S., Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                         AG247247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTCTGCCCATCATCACCTTCGTGGACACGCCCGGAGCCTATGCCGGCAAGACCGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCGCCATCCTGTGGGAAGAGCCGCTCTGCCGCCGGCGAGGCCACTGAGGCCCTGCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGC 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGCTGGGCCAGGGCCATTGCCGTGAACCTGCGTGAGATGTTCGGCCTGCGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines CDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
synthesized. The cDNA was directionally cloned to lambda
synthesized. The cDNA was directionally cloned into lambda
synthesized. The BCORI (5') and XhoRI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
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/clone_lib="C_reinhardtii CC-1690,
), Lambda_Zap_II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript II SK-; Site_1:
                                                                                                                                                                                                                                                                                                                                         GI:26647012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.7%;
51.0%;
                                                                                                                                                                                                                                                                                                                                                                                    DNA, clone:LjT20k03_not, genomic survey sequence.
                                                                                     and Tabata, S
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Pred. No. 2.3e-11;
0; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                   652 bp
                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201;
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RESULT 12
CB977199/c
                                                                  REFERENCE
                                                                                                                                                                    SOURCE
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                                                                                                                                                                                                                              617 bp mRNA linear EST 01-MAY-200:
CAB40003_IVa_Ra_D11 Cabernet Sauvignon Berry - CAB4 Vitis vinifera
CDNA clone CAB40003_IVa_Ra_D11 3', mRNA sequence.
CB977199
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                                                              Spermatophyta; Magnoliophyta; Vitaceae; Vitis.
1 (bases 1 to 617)
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
                                            Goes
                                                                                                                                             Vitis vinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato, S.
Direct Submission
                                                                                                                          Eukaryota; Viridiplantae;
                                                                                                                                                                    Vitis vinifera
                                                                                                                                                                                                           CB977199.1 GI:30300405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTTGGTGAAAACTG 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTGGGTCCTCGCGTGGTGGTAGT 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTGATTGATGGAATTGTGTCGC 1159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTATTTGCGCAA----TCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTTCATCTGGGC 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recreercreccrecrreceerecrecececarecaeeaaeaacaarcaaecrrrrerca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGTÄTTCCTGTAGCAATTGGGATTATGGATTTTTGAGTTATGGGAGGTAGTATGGGAT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                          da Silva, F.,
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/clone="LjT20k03 not"
/clone_lib="genomic TAC library"
/note="VECTOR:pYLTAC7"
/note="VECTOR:pYLTAC7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Lotus japonicus"
|mol type="genomic DNA"
|strain="Miyakojima MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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                                        Iandolino, A., Lim, H.,
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Pred. No. 4.5e-11;
0; Mismatches 219;
                                                                                                  Streptophyta; Embryoyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                 515
                                        Baek, J., Jones, K. and Cook
                                                                                                                            Embryophyta; Tracheophyta;
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UC Davis, Plant Pathology
One Shields Ave, Davis, CA 9
Tel: 530 754 6561
Fax: 530 754 6617
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Contact: Douglas Cook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 berries at various developmental stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGGGGGTAGTATGGGATCCGTAGTAGGTGAGAAAATTACCCCGTTTGATCGAATATGCC
    GGTAAAAGGGTAATTGAACAAACATTGAAAAAGACAGTACCTGAAGGGTTCACAAGCGGCT
                                        GETECTEGEGEGEGEGETAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCG 1116
                                                                                   AGTTTTGGTATGTTGGGAGATATCATTATTGCCGAACCCAATTCCTACATTGCATTTGCG
                                                                                                                            TCGTGGGGTTCATCTGGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTG
                                                                                                                                                                    AATAAAAAGTTATTTTATGTATCAATCCTTACATCTCCTACTACTGGTGGGGGTGACAGCA
                                                                                                                                                                                                           GCGCATTTGCCGTTCCTGGTGTATTTGCGCAA----TCCCACGATGGGTGGCGCCATGGCC
                                                                                                                                                                                                                                                      GACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAG
                                                                                                                                                                                                                                                                                                                                 ACCAATGAATTTCTACCTCTTATTTTAGTGTGTTCTTCCGGAGGAGCACGTATGCAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AMGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and 5'-ATTCTAGACGCCGACGGCCGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction." a 129 c 94 g 203 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Cabernet Sauvignon Berry - CAB4"
/note="Organ: Berry; Vector: pDNR; Size_1: Sfi; Site_2:
Sfi; CAB4 is a cDNA library of Vitis Vinifera cv.
Cabernet Sauvignon' Clone 8 berries. Sampled berries were collected from field-grown vines during stage II of berry growth (berries were green and hard) at approximately 60 days after full bloom. The average berry size was 9 milimeters. Sampled vines were located at the University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Hermaphrodite"
/dev stage="Berry on stage II,
/lab_host="DH5alpha"
/clone_lib="Cabook"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:29760"
/clone="CAB40003_IVa_R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Vitis vinifera"
/mol_type="mRNA"
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47.8%;
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Pred. No. 2.5e-10;
0; Mismatches 270;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvi.
Tel: (301)-838-3529
Fax: (301)-838-0208
       BZ035752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 668)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M.,
Kerlavage,A.R. and Adams,M.D.
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Mammalia; Eutheria;
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                                                                                                                                                                                       GAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATT
                                                                                                                       TGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCG 988
                                                                                                                                                       TGTCGCTGATGCAGATGGCGAAAACCTCTGCGGCACTGGCAAAAATGCAGGAGCGCGGCT
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                                                                                                                                                                                                                                                                                                                                                              AAGGCACTCTGTATGGAATGCCGGTTGTCGCTGCGGCATTCGAGTTCGCCTTTATGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 Normalized rat embryo, 37 end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus sp."

mol type="mRNA"

/db_xref="ATCC (inhost):2036524"

/db_xref="taxon:10118"

/clone="REMCJ63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pTTT1Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pTTT1Pac; Site_1: EcoRI; Site_2: NotI"
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Pred. No. 5.2e-10;
0; Mismatches 130;
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1055 TGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGG 1114
                                                                  995
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                                                                                                      242
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BZ035752
BZ035752.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (Dases 1 to 677)

Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      washington University School of Medicine Email: submissions@watson.wustl.edu Plate: oeh49 row: c column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 8
High quality sequence stop: 551
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea
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                               CAAGTTTTGGTATGTTGGGGGATATCATTATTGCCGAACCCTATGCCTACATTGCATTTG 123
                                                                                                  CAAGTAAAAAGGTATTCTATATATCAATTCTTACATCTCCTACTACCGGTGGGGTGACAG
                                                                                                                                                                   AAGGAAGTTTAAGTTTGATGCAAATGGCTAAAATTTCTTCGGTTTTATGTGATTATCAAT
                                                                                                                                                                                                   AAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCG
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                                                                 CCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGGGGGGAAAGGTTTCC
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
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Pred. No. 6e-10;
0; Mismatches 283;
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oeh49c05.g1 B.oleracea002 Brassica oleracea genomic, genomic survey

Whole genome shotgun reads from Brassica oleracea Unpublished

/clone lib="B.oleracea002"
/note="Vector: pOTw013; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000H3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

Indels Length ω •• Gaps

1054 183 243 937

877 363 817 423 757

O; Mismatches	
Score 73.6; DB 14; Length 606; Pred. No. 6.4e-10; 0: Mismatches 269; Indels 3:	Query Match Best Local Similarity 47.7%; Matches 248: Conservative
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Facility Lant Pathology Ave, Davis, CA 95616, USA 4 6561 4 6617 5 6617 ACGGTACCGGACATATGCC. ACGGTACCGGACATATGCC 606 - 606 - 606 - 608	ome Fac , Plant 1ds Ave 754 65 754 66 rcook@u er: ACC er: ACC Locati 160
uence tags from cabernet sauvignon berries at various stages 03 this sequence version replaced gi:28967937. las Cook. PhD	ressed sequelopmental aublished Mar 14, 20, tact: Dougle
<pre>idiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids tis. 606) 606) 6., Tandolino, A., Lim, H., Baek, J., Jones, K. and Cook</pre>	Vitis vinifera Eukaryota, Vir Spermatophyta, 'Vitaceae; Vi E 1 (bases 1 to S Goes da Silva,
606 bp mRNA linear BST 10-APR-2003 VaF_C02 Cabernet Sauvignon Berry - CAB2SG Vitis A clone CAB2SG0002_IVaF_C02 5', mRNA sequence.	RESULT 15 CB346970 LOCUS CB346970 CB2FINITION CAB2SG0002 IVAF C02 VINIFERA CDNA Clone ACCESSION CB346970 CES46970 CES46970 CES46970.2 GI:2978: KEYMORDS EST.
	1175 CA 1176 2 CA 1
CGGAGAATTTGGTGAAAACTGGTGTGTGATTGATGGAATTGTCGCCACTCCAATTGCGTG 1174	1115 CGGAGAATTTGGT
	 122 CGGGTAAAAGAGT

Search completed: November 13, 2003, 02:26:29 Job time : 4682.43 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-252-991A-12180

US-09-252-991A-12415

US-09-252-991A-12365

US-09-107-532A-170

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ALIGNMENT

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; NAME/KEY: gene
; LCCATION: (508)...(1980)
; OTHER INFORMATION: accDA
US-09-362-899-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09362899

Patent No. 6361986

GENERAL INFORMATION:

APPLICANT: Degussa-H1s AG

APPLICANT: Porschungszentrum-J1ich GmbH

TITLS OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY FERMENTATION IN CURRENT APPLICATION NUMBER: US/09/362,899

CURRENT FILING DATE: 1999-07-29

EARLIER APPLICATION NUMBER: DE 19924365.4

EARLIER FILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 2123; Best Local Similarity 100.0%; Pred. No. 0; Matches 2123; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Corynebacterium glutamicum FEATURE:
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; FEATURE:
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                                                                                                                                                                         Sequence 2, Application Patent No. 6361986 GENERAL INFORMATION:
                                                                                             APPLICANT: Degussa-Hls AG
APPLICANT: Forschungszentrum-Jlich GmbH
TITLE OF INVENTION: PROCESS FOR THE PREPARATION
CURRENT APPLICATION NUMBER: US/09/362,899
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: DE 19924365.4
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches
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DЬ	γQ	Ф	Ş	Дb	V	Db	Q	Db	Qy	DЬ	γQ	Db	Q	Дb	δ
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		1440	1947	1380	1887	1320	1827	1260	1767	1200	1707	1140	1647	1080	1587

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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF BEQ ID NOS: 2
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; Sequence 2, Application US/09103840A
; Patent No. 6294328
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Best Local S
Matches 717
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                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
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TYPE: DNA
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CGATCGTGTTCCGAGACACTGCTCATGCCGCCGAACTCGCTGCCGCCCAAGGCATCCGGT 1006892
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; CRGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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US-09-103-840A-1/c
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APPLICANT: FLEISCHMAN, Robert
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09103840A Patent No. 6294328
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRA
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.000
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                TCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGC 1111
                                                                                           TGGCCTCGTGGGGTTCATCTGGGGCATCTCACTTTTGCGGAACCCGGCGCCAGATAGGTT
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US-08-311-731A-140
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                                                                                                                 Sequence 140, Application US/08311731A
PATENT NO. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                      NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS,
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US-08-311-731A-140
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Best Local Similarity
Matches 296; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
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MOLECULE TYPE: DN
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: circular
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
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GGACTGCAACTGACGTTGAATCGTGCGCTGACGATGAT 31940
                                                 CAATTGCGTGCAGCGGTGGCAAAAACCCCTCAAGGTTAT 1202
                                                                                                                                                                                                                                            ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT 1104
                                                                                                                                                                                                                                                                                                                                                          GGCGCCATGGCCTCGTGGGGTTCATCTGGGGATCTCACTTTTGCGGAACCCCGGCGCGCAG 1044
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                                                                                                                                                       ATCGGCTTCCTTGGGCCTCGGGTGTATGAGTTGCTGTATGGCGAACCTTTCCCGTCCGAC
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12180
LENGTH: 1020
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US-09-252-991A-12415/c
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                                                                                                       GENERAL INFORMATION:
                                                                                                                            Sequence 12415, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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ORGANISM: Pseudomonas aeruginosa
-09-252-991A-12180
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TITLE OF INVENTION: NUCLEIC ACID AND AND ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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              APPLICANT: Khosla, Chaitan
TITLE OF INVENTION: NON-STROGEN-R
TITLE OF INVENTION: ANTAGONISTS
FILE REFERENCE: 28600-20210.00
CURRENT FILING DATE: 2000-06-08
FRIOR APPLICATION NUMBER: US 60/243,458
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 60/179,305
PRIOR APPLICATION NUMBER: US 60/179,305
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 23673
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US-09-773-816-1/c
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APPLICANT: Stanford University
APPLICANT: Khosla, Chaitan
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     TYPE: DNA
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ESTROGEN-RECEPTOR

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US-09-252-991A-12415
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12415
LENGTH: 1338
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Local Similarity 52.0%;
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                                           AATTGCGTGCAGCGGTGGCAAA 1187
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                                                                                      TCCAGCGTAGCGAGTTCCTTCAGCATGGCGCCATCGACATGATCGTGCATCGTGCCCG
                                                                                                                                 Conservative
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Pred. No. 3.1e-24;
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Best Local S
Matches 611
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(23623)
OTHER INFORMATION: n = A,T,C
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 CGAGCTAAACCTGCCGATCGTGTCCATCGATCGCGCGGCGCCGAATTGTCGCAGGC
                                                   CTTCGGCATGCCGATCCCGTCGGGCTACCGCAAGGCCGCCCGGATCATGCGGCTCGCCGA
                                                                                   CICCETTICCCCI
                                                                                                                  ACCCGTCGCCGTCATCGGCCACCAGAAGGGCCACGACGCGCAGGAGCTGCGCCGCCGAA
                                                                                                                                                    GCCCGTGGTGCTGATTGGGCA-----
                                                                                                                                                                                 CGACCGCATCTCGGGCGACTGCCCCGCCATCGTCGCCGGCCTGGCCCGCCTTCGGCGGCCG
                                                                                                                                                                                                                                                  CCGGCCCACCACGACTACATCGCGCTGCTGCGAGGACTTCGTCGAACTGCGCGG
                                                                                                                                                                                                                                                                               -- GGCCTGGAATCGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAGCTTTCTGG
                                                                                                                                                                                                                                                                                                                                                CAACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTGACCCGCAGA
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Pred. No. 2.7e-21;
0; Mismatches 619;
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US-09-107-532A-170
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GENERAL INFORMATION:
                                                                                                                                               INFORMATION FOR SEQ ID NO: 170:
                                                                                                                                                                                            APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TOPOLOGY: circular MOLECULE TYPE: DNA (genor HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 870 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7:
CORRESPONDENCE ADDRESS
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                                                                                                                                                               TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGGTCACCGCCGCGAACTCCTCGGCCTGGGCATCGTCGACGGCGTCCTCCCGGAACC
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                                                                                  STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASC:
                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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                                                 (genomic)
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and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAF

THERAPEUTICS

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7307

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;
NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...870;
SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-09-107-532A-170
                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-252-991A-12365/c
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                                                         ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12365
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                                                                                                                     SEQ ID NO 12365
                                                                                                                             APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEG ID NOS: 33142
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity
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 Matches
                            Query Match
                                                                                          TYPE: DNA
               Local Similarity
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              807
              4.6%;
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Pred. No. 1e-20;
0; Mismatches 2
              Score 97.2; DB 4;
Pred. No. 8.2e-19;
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles K
                                           TELEPHONE: (301) 309-8512
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: *
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
LENGTH: 19702 base
TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                    COMPUTER: HP Vect
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
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                                                                               MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NOMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: Unknown>
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   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
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ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                         STATE: MD
                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTACCAGATACGATTGCTA 11053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG
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                                                                                                                                                                                                                     ZIP:
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Pred. No. 1.1e-17;
0; Mismatches 253;
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                                                                                                                                                                         Sequence 1, Application Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Rober
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Best Local
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                 Application US/09643990A
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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REGISTRATION NUMBER: 41,971
                      Owen White
Owen White
Hamilton O. Smith
J. Craig Venter
OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
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                                                                                                                                                                             Robert D. Fleischmann
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Pred. No. 1.2e-16;
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Fragments

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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-643-990A-1
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FILING DATE: 1995-06-07
APPLICATION UMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: KENLEY K. HOOVET
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEPHONE: 301-610-5790
TELEPHONE: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
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Best Local :
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MEDIUM TYPE: 3 1/2 inch disket:
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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248; Conserv
AATTGCGTGCAGCGGTGGCAA 1186
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                                                                TCCAACGTAGTGAGTTTCTACTTGAGAAAGGGGCAATTGATATGATCGTGAAACGTTCAG 1337459
                                                                                                                                                                                                                                                                                                                             CTCAAATGCGTGAAAAGGGTGTGCCATTTATTTCAGTATTAACGGATCCGACTTTAGGCG
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
                                                                                                         TTGGTTTTGCAGGGCCACGCGTTATTGAACAAACTGTGCGTGAAAAATTGCCAGAAGGTT
                                                                                                                                                                                           TAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG
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Pred. No. 1.2e-16;
0; Mismatches 253;
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US-09-347-878-25
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Best Local Similarity
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TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
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DATABASE ACCESSION NUMBER: M32445/GenBank
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LOCATION: (1131)..(2399)
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                          TAGTGGTACCCCCGGTACCGGA
                                                                GCGTGGCACTTCCGGTGATGGA 1268
                                                                                                                                                   ANACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACTCCTG 1246
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                                                                                                                                                                                                TCGAGAAAGGCGCGATCGACATGATCGTCCGTCCGGAAATGCGCCTGAAACTGGCGA
                                                                                                                                                                                                                                      TGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAA 1186
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                                                                                                         GCATTCTGGCGAAGTTGATGAATCTGCCAGCGCCGAATCCTGAAGCGCCGCGTGAAGGCG
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US-08-973-275-2
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CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: PCT/JP97/01043
EARLIER FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: JP 8-97536
EARLIER FILING DATE: 1996-03-28
EARLIER APPLICATION NUMBER: JP 8-146833
EARLIER FILING DATE: 1996-05-16
NUMBER: OF SEQ ID NOS: 6
CONTINUES: DATE: 1996-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.1
Best Local Similarity 33.6
Matches 152; Conservative
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SEQ ID NO 2
LENGTH: 954
TYPE: DNA
ORGANISM: Magnetospirillum AMB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08973275B Patent No. 5958706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FINE MAGNETIC PARTICLES CONTAINING USEFUL PROTEINS TITLE OF INVENTION: BOUND THERETO, PROCESS FOR PRODUCING THE SAME, AND USE TITLE OF INVENTION: THEREOF FILE REFERENCE: MATSUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:

NAME/KEY: gene
LOCATION: (217)..(702)

OTHER INFORMATION: Predicted region encoding membrane bound portion
OTHER INFORMATION: of the mps gene product. "n" is any of a, t, c or
OTHER INFORMATION: g.
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APPLICANT: KAMIYA, Shinji
APPLICANT: NAMBA, Kenryo
                                                                                                                                                                                                                                                                                                           1698 GGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGGCGCCTCGGCCAT 1757
                                                                                                                                1818 CGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGA 1877
                                                                                                                                                                                                                        1758 ССТСТТСССССВАСАССААССАСССССССССВАЛАТСАТАСАСССВАСБАСССТССВСССССВ 1817
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YMGNAAYCCNGAYYTNATGATGCARACNYTNWS
                                        AGAAATTCTCGGCACAATCAGCAACGCCCTCTC 1910
                                                                                   RGAYYTNCAYAARYTNWSNATHATHGAYWSNGTNGTNCCNGARCCNATGGGNGGNGCNCA
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Search completed: November 13, 2003, 00:14:44

Job time : 166.654 secs



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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2123
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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SUMMARIES
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		n	n	Result
14 16	13111	00 7 6 5 4	321	197
97.8 96.8 96.2	121 119.2 119.2 108 102.8	14/3 312.6 131 122.8 122.8	2123 2111 1473	Score
4.4.4 0.00		14.7 6.2 5.8	100.0	Query
867 654 891	6021 870 1053 993 915	1488 1488 354 873 867	2123 3309400 1473	Query Match Length DB
9019	99196	9 2 1 5	13	
US-09-815-242-9520 US-09-974-300-5531 US-09-815-242-7115	US-09-070-927A-458 US-09-815-242-7288 US-09-895-913A-97 US-09-815-242-9854 US-09-815-242-6133	US-09-712-363-35 US-09-712-363-35 US-09-738-626-3442 US-09-815-242-7800 US-09-815-242-6828	US-10-024-370-1 US-09-738-626-1 US-09-738-626-929	ID
Sequence 9520, Ap Sequence 5531, Ap Sequence 7115, Ap	Sequence 458, App Sequence 7288, Ap Sequence 97, Appl Sequence 9854, Ap Sequence 6133, Ap	Sequence 2, Appli Sequence 35, Appl Sequence 342, Ap Sequence 7800, Ap Sequence 6828, Ap	Sequence 1, Appli Sequence 1, Appli Sequence 929, App	Description

45	C 44	43	42	41	40	39	38	37	c 36	35	34	33	32	31	c 30	29	28	27	26	25	C 24	23	22	21	20	19	18	1.1
43.4	44.4	44.8	45	45.8	46	46.2	48.2	48.6	48.6	49.8	49.8	49.8	52.6	54.6	56.4	57.2	59.6	59.6	67.8	67.8	79	79	81.8	84.8	85.2	86.4	93	20.4
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US-10-289-757-151	US-10-162-497-7	US-10-156-761-7101	US-10-156-761-2173	US-09-815-242-4026	US-09-841-132-461	US-10-003-446-14	US-09-767-479-11	US-10-156-761-3330	US-09-815-242-2856	US-10-156-761-3349	US-09-815-242-9521	US-09-815-242-9268	US-09-815-242-9799	US-09-815-242-5951	US-09-070-927A-269	US-09-974-300-1085	US-09-815-242-3909	US-09-815-242-6829	US-10-156-761-1	c	US-10-156-761-1	US-10-156-761-5702	US-09-815-242-7836	US-08-781-986A-312	US-09-815-242-4369	US-09-815-242-8520	US-09-815-242-9267	CO FO 187 700 F
Sequence 151, App	Sequence 7, Appli	Sequence 7101, Ap	2173	Sequence 4026, Ap	Sequence 461, App	Sequence 14, Appl	Sequence 11, Appl		Sequence 2856, Ap	Sequence 3349, Ap	Sequence 9521, Ap	Sequence 9268, Ap	Sequence 9799, Ap	Sequence 5951, Ap	Sequence 269, App	Sequence 1085, Ap	Sequence 3909, Ap	-	Sequence 1, Appli	Sequence 3318, Ap	Sequence 1, Appli	Sequence 5702, Ap	7836,	Sequence 312, App	4369,	8520,	Sequence 9267, Ap	riddu 'r pomping

ALIGNMENTS

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PRIOR APPLICATION NUMBER: 09/362,899
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2123
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: gene
LOCATION: (508)..(1980)
OTHER INFORMATION: accDA
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US-10-024-370-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: TILG, YVONNE
APPLICANT: ELKMANNS, BERND
APPLICANT: EGGELING, LOTHAR
APPLICANT: SAHM, HERMANN
                                                                                        Query Match 100.0%; Score 2123; Best Local Similarity 100.0%; Pred. No. 0; Matches 2123; Conservative 0; Mismatches
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MOCKEL, BETTINA
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
TITLE OF INVENTION: FERMENTATION AND NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: accdA GENE
FILE OF INVENTION: accdA GENE
FILE REFERENCE: 21123-284139-MAS
CURRENT EPPLICATION NUMBER: US/10/024,370
CURRENT FILING DATE: 2001-12-21
CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA
                          CTCGAGCGGGAGTCGGTGATCGGCCACTCTCTAAGCAATGCCGGCTTTAAAATAAAGCAA
                                                                                                                                      DB 13;
                                                                                        0
                                                                                                                                    Length
                                                                                                                                      2123;
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  60
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1081 ACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGCGGAGAATTTGGTGAAAACTGGTGTG 1140 	61 CTTATATATGTTTCTCACCACATCTGGCCGACGACGACCACCACGACGACCACCACGACGACCACC	
RESULT 2 US-09-738-626-1/c ; Sequence 1, Application US/09738626 ; Publication No. US20020197605A1	ON 1111 ATTOCHOCOCCOCCANACCOCCANACCOCCOCCANACCOCCOCCANTOCCCCA 114 ATTOCHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1111 1000000000000000000000000000000000

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APPLICANT: ANDO, SELAN
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILLE REFERENCE: 249-125
FILLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: JP-94/377484
PRIOR APPLICATION NUMBER: JP-94/377484
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP-09/159162
PRIOR APPLICATION NUMBER: JP-09/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VOT. 3.0
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
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APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
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                                 ATGGAACACACTTCAGCATTGACGCTCATAGACTCGGTTTTGGACCCTGACAGCTTCATT
                                                                                                                                                               TCGATAGCCTAAATTGGGCTTAGATCTTCCGCCTCTAAATAGGTATGCAGAGACATTCGA 480
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Sequence 929, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
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Best Local Similarity
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
APPLICANT: Marcotte, Edward M.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY
FILE REFERENCE: 07/419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: FOT/US00/02246
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR APPLICATION NUMBER: 60/118,206,
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US-09-712-363-35
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Patent No. US20020164588A1
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SOFTWARE: FastSEQ for Windows Version
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                                                                           CGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTG
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3442
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 9/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari L.
APPLICANT: Zyekind, Judith w
                                                                                                                                                                                                                                                                   Sequence 71 Patent No.
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LENGTH: 354
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Best Local Similarity
                                                                                                                                   APPLICANT:
APPLICANT:
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     FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                        APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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o. US20020061569A1
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Trawick, John D.
                                                                                                                                 Carr, Grant J.
                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
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SENOH, AKIHIRO
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Pred. No. 2.1e-32;
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PRIOR FILING DATE: 2000-10-23
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
Sequence 6828, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:
NAME/KEY: CDS
LOCATION: (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 5.8%;
Local Similarity 52.8%;
les 265; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746 CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG
                                                                                                                                                                      AGTTGCGGCCGCCCTGGCCAA 827
                                                                                                                                                                                                       AATTGCGTGCAGCGGTGGCAAA 1187
                                                                                                                                                                                                                                                                                                                                              TAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG 1105
                                                                                                                                                                                                                                              TCCAGCGTAGCGAGTTCCTCCTTGAGCATGGCGCCCATCGACATGATCGTGCATCGTGCCG
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                                                                                                                                                                                                                                                                                                                       TCGGCTTCGCCGGTCCTCGCGTGATCGAGCAGCAGCCGTCCGCGAGAAGCTTCCGGAAGGCT
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Pred. No. 2.1e-29;
0; Mismatches 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0
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US-09-815-242-6828
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 259;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (1)...(867)
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ORGANISM: Enterococcus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 867
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R FILLING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR FILLING DATE: 2000-11-27
DR APPLICATION NUMBER: 60/257,931
DR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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1165 CAATTGCGT 1173
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                                                                                748 TTTCAAAAGGCCGAGTTTCTTTTAGAACATGGTTTTGTAGATCAGATTGTGCCAAGAAAT 807
                                                                                                                                                                                                                                                     889
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                                                                                                                                                            ATCGGTTTTGCTGGCCGCCGTGTAATTGAACAAACGATTCGTCAAGAGTTGCCAGATGAT
                                                                                                                                                                                                                                                                                                                         ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT 1104
                                                                                                                                                                                                                                                                                                                                                                                                             GGTGTTACCGCAAGTTTTGCGATGGATGGCGATATTATTTTGGCAGAGCCTCAGAGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 8.3e-29;
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SEQUENCE DESCRIPTION: SEQ ID US-09-070-927A-458
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US-09-070-927A-458
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 458: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,655

FILING DATE: 1997-05-16

APPLICATION NUMBER: 60/044,031

FILING DATE: 1997-05-06

APPLICATION NUMBER: 60/066,009

FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MCDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
COPERATING SYSTEM: MSDOS version 6.2
 5501
                                                                                                                                                                                                                                   5321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,3
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Charles A. Patrick J.
                                                                                                                                                     5381 ATGGACGCTAATTTTATCATGGGCAGTATGGGAACGATTGTTGGTGAAAAAATCACACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
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                                                                                                                                                                                                                                                                     685 GATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTG
                                                                                                                                                                                                                                                                                                             259;
                                                                                                                                                                                                                                   GATGAAGCTGTCTTAACGGGAGAAGCAACAATTGAAGGACAAGCTGTTGCAATTGGAATC 5380
 GCCCGTATGCAAGAAGGAATTTTTTCATTGATGCAAATGGCGAAAATTTTCGGCCGCTTTG
                                   GCGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTG 924
                                                                           TTGTTTGAGCGGGCGACAGAAAAGCATTTACCAGTAGTGATTTTCACTGCATCTGGTGGT
                                                                                                                 GCGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGT
                                                                                                                                                                                           TCCGATTTTTCCTTCCTCGGCGCTTCTTTGGGCACGCTCGCGTCGCGCATCATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 6021 base pairs
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                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                         Score 121; DB 10;
Pred. No. 3.1e-28;
0; Mismatches 230;
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EENGTH: 870

TYPB: DNA
OGGANISM: Helicobacter p
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(870)
US-09-815-242-7288
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
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                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7288
                                                                                                                     Matches
                                                                                                                                        Query Match
Best Local
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes
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                                                                                                                                    h 5.6%;
Similarity 50.9%;
                                    TTTACGGCCTAATGATCCTTTAAATTTCGTGGATAAAGAGAGCTATAAACAACGCATTAA
                                                                           CTTTTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu, H. Howard
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                                                                                                                   Conservative
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                                                                                                               Score 119.2; DB 9;
Pred. No. 3.3e-28;
0; Mismatches 273;
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; LOCATION: (110)...(976)
US-09-895-913A-97
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                                                                                                                                                                                                                                                    FILE REFERENCE: 06132/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/09895913A
Patent No. US20020160456A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
                                                                                 Query Match
Best Local Similarity
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456A1el Helicobacter Polypeptides in
TITLE OF INVENTION: Genome
                                                                                                                                                                                    LENGTH: 1053
TYPE: DNA
ORGANISM: Helicobacter
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1020
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Tomb, Jean Francois
                                                                 5.6%; ilarity 50.9%; Conservative
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Pred. No. 3.8e-28;
0; Mismatches 273;
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9854
LENGTH: 993
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                     PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                        APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                              APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                                                       FILING DATE: 2000-12-22
                                                                                                                        FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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Zyskind, Judith W.
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FEATURE:
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Local Similarity 49.6%;
nes 276; Conservative
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AGCTGGCGAGCATTCT
                                                                                 AGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAG
                                                                                                                                                   GTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGG
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                              CGGTGGCAAAAACCCT 1193
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                                                         AGTTCCTGATCGAAAAAGGCGCTATTGATATGATAGTCCGCCGTCCGGAAATGCGCCTGA
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US-09-815-242-6133

Sequence 6133, Application US/09815242

Patent No. US20020061569A1

GEMERAL INFORWATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karii L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: 00/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

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RESULT 14
US-09-815-242-9520
; Sequence 9520, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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Best Local Similarity
Matches 275; Conserv
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ORGANISM: Escherichia c
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(915)
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Pred. No. 9.9e-23;
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NAME/KEY: CDS
LOCATION: (1).
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER: 0F SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 9520
LENGTH: 867
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Zyskind, Judith
Wall, Daniel
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Pred. No. 4.4e-21;
0; Mismatches 252;
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451 805

511 865

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691

985 571 925

631

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LENGTH: 654

TYPE: DNA

GRANIAN: Bacillus clausii

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(654)

OTHER INFORMATION: n = A,T,C or G

US-09-974-300-5531
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085-500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.6%;
Best Local Similarity 51.8%;
Matches 288; Conservative
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CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
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                                  1112 AGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGC 117:
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Pred. No. 7.8e-21;
0; Mismatches 264;
                                                                         CAGGAACTTCCTGAAGACTTTCAGA
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Search completed: November 13, 2003, 06:16:26 Job time : 1310.22 secs

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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR202320	RESULT 1
nucleotide sequences coding for the accDA gene Patent: US 6361986-A 2 26-MAR-2002;	Process for the preparation of L-amino acids by fermentation and	Tilg,Y., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel,B.	1 (bases 1 to 1473)	Unclassified.	Unknown.	Unknown.	•	AR202320.1 GI:20256859	AR202320	6.	AR202320 1473 bp DNA linear PAT 20-APR-2002		

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Query Match Best Local Matches 147	FEATURES SOURCE BASE COUNT ORIGIN		AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 3 BD004742 LOCUS DEFINITION	Qy 14 Db 14	Qy 1381 Db 1381	Qy 1321 Db 1321	Qy 1261 Db 1261	Qy 12 Db 12
y Match 100.0%; Score 1473; DB 6; Length 1473; Local Similarity 100.0%; Pred. No. 6.7e-293; nes 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CDS Location/Qualifiers 11473 . /organism="Corynebacterium glu/mol_type="genomic DNA" /bb_xref="taxon:1718" 275 a 414 c 456 g 328 t	PN JP 2001008693-A/2 PD 16-JAN-2001 PF 14-MAY-2000 JP 2000153547 PF 24-MAY-2000 JP 2000153547 PR 27-MAY-1999 DE 19924365.4 PI IVENNE TILKE,LOTHAR EGGERING, BERNHARD EICKMANS, HERMANN ZAMU, PI VETTYNA MCKEL PC C12P13/09, C12N1/21,C12P13/04,C12P13/06,C12P13/06,C12P13/08, PC C12P13/09 PC C12P13/12,C12P13/20,C12P21/02//(C12N15/09,C12R1:15),(C12N1/21, PC C12P13/04,C12R1:15),(C12P13/06,C12R1:15),(C12P13/06,C12R1:15),(C12P13/06,C12R1:15), PC (C12P13/12,C12R1:15),(C12P13/06,C12R1:15),(C12P13/06,C12R1:15), PC (C12P13/12,C12R1:15),(C12P13/20,C12R1:15),(C12P13/06,C12R1:15), PC (C12N15/00,C12R1:15) PC (C12N15/00,C12R1:15) CC Location/Qualifiers	Tilke, I., Eggering, L., Eickmans, B., Zamu, H. and Meck, V. Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector, and process for producing L-amino acid Patent: JP 2001008693-A 2 16-JAN-2001; DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUBLICH GMBH OS COrynebacterium glutamicum	BD004742 BD004742.1 GI:18632703 BD004742.1 GI:18632703 JP 2001008693-A/2. Corynebacterium glutamicum Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium. 1 (bases 1 to 1473)	BD004742 1473 bp DNA linear PAT 31-JAN-2002 Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector, and process for producing L-amino acid.	.41 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1473 	81 GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGAGGGCGGGACGCGAC 1440 	21 AGCCAAGGGCTTATCGACGGGATCGTCGCCCGAAACCGAGCACTTTGTTGAAGAAATTCTC 1380	61 GACACCAACCACGCGGGAAATCATAGAGGCGACAAGGCGTGCAGGCGCACGCA	01

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Patent: JP 2002191370-A 929 09-JUL-2002;

KYOWA HAKKO KOGYO CO LTD

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PN JP 2002191370-A)929

PD 09-JUL-2002

PF 15-DEC-2000 JP 2000405096

PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SE:
PI KEIKO OCHIAI,
PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO
PI OZAKI
PC C12N15/09, C12N15/09, C07K14/34, C07K16/
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Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A. Novel polynuclectide
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SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
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                                              /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pompejus,M., Kroeger,B., Schroeder,H., Zel
corynobacterium glutamicum genes encoding
membrane synthesis and membrane transport
Patent: WO 0100805-A 25 04-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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IDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVY
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                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-JUN-1998) |
California at Berkeley, |
Lab, | 111 Koshland Hall, |
Related sequence x66112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim, K., Pete
Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGL17592 2123 bp DNA linear BCT Corynebacterium glutamicum accDA gene. Y17592 1GI:14572581 accDA gene; acetyl-CoA carboxylase; carboxyltransferase. Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteria; Actinobacteria;
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Peters-Wendisch, P.G.
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/strain="AFTC 13032"
/db xref="taxon:1718"
508. 1983
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/trainalation="Mekreptmymgmehtsaltlidsvldpdsfismnetpqydnlnq/lyafterarskakcdesvitgegtyrgipvavilldpdsfiscaticatikalih gyaettlerarskakcdesvitgegtyrgipvavilldpfsficasletikuselkakcdesvitgegtyrgiptavotatikalih gyaettlivspasggarmapsmarfymmysitaavdrherahlpflyvllnptmggamaswgssghiltfarpgaqigetigrryvetytgtalpvmeaiarsrdpqregigeimetlgadurkakvaktilkviqpveatdrfspttgvalpymeaiarsrdpqregigeimetlgaduvklsgaragalspavrvalariggrpvvlligqdrrftlgpqelrfarrgislarel
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/trans1_table=11
/product="putative carboxyltransferase subunit
/protein_id="CAC42827.1"
/db_xref="GI:14572582"
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                    GGGGGCCGGCCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGCTTCGGCCGCAGGAG
                                                      CTTTCTGGTGCGCGTGCTGCGCCATTGAGCCCGGCTGTGCGC
                                                                 CTTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCTGGCGCGCATC
                                                                                                         GACCCGCAGAGGCCTGGAATCGGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAG
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Tilg,Yr., Eikmanns,B., Eggeling,L., Sahm,H. and Mockel,B.
Process for the preparation of L-amino acids by fermenta
nucleotide sequences coding for the accDA gene
Patent: US 6361986-A 1 26-MAR-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Unknown.
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AACCTCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCAAGGCCAAATGCGAT
                                                      ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCCAATATGAC
                                                                                         GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC
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Qy	Q y Db	Query Ma Best Loc Matches	JOURNAL COMMENT FEATURES SOURCE SOURCE ORIGIN	RESULT 8 BD004741 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	
61 ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGAC 120	1 GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC 60	Match 100.0%; Score 1473; DB 6; Length 2123; Local Similarity 100.0%; Pred. No. 6.4e-293; les 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PATENT: JP 200100893-A 1 16-JAN-2001; DEGUSSA HUELS AG. FORSCHINGSZENTRUM JUELICH GMBH OS COTYNEDACTETIUM GIUTAMICUM PN JP 2001008693-A/1 PN JP 2001008693-A/1 PN JP 2001008693-A/1 PN JP 2001053547 PR 27-MAY-2000 JP 2000153547 PR 27-MAY-1999 DE 19924365.4 PI IVENNE TILKE, LOTHAR EGGERING, BERNHARD EICKMAP PI VETTYNA MECKEL PC C12N15/09, C12N1/21, C12P13/04, C12P13/06, C12P13/08 PC C12P13/08, C12N1/21, C12P21/02//(C12N15/09, C1:P13/04, C12P13/06, C12R1:15), (C12P13/06, C12R1:15),	BD004741 BD004741 BD004741 Replicable DNA, amino acid sequence, Corynebacterium microorganism, shuttle vector, and process for producing L-amino acid. BD004741 BD004741.1 GI:18632702 JP 2001008693-A/1. Corynebacterium glutamicum Corynebacterium glutamicum Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales; Corynebacterineae; Corynebacteriumee, Corynebacteriumee, Corynebacteriumeen, Eickmans, B., Zamu, H. and Meck, V. Replicable DNA, amino acid sequence, Corynebacterium and not acid.	GACACCAACCACCACCGCGGAAATCATAGAGCGACACACCAACCA

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GETTGAAGCAAGGCAATTGCGAT ATTCCGGTAGCAAGCCAATTGCGAT ATTCCGGTAGCAAGCCAATTGCGAT ATTCCGGTAGCCAAGCCA	141 ATTGGTCAGGGCGTTGGCGGTTGGCGATV	5 0	1021 ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCG	961 CTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGCG	901 GGGGCCCGGCCCGTGGTGCTGATTGGGCAGGATCGC	41 CTTTCTGGTGCGCGTGCTGGCGCAT	81 GACCCGCAGAGGCCTGGAATCGGGG 	21 TTTTCTCCAACACTCCTGGCGTGG 	61 TTGCGTGCAGCGGTG	01 CAGCAGGCGGAGAAT	41 GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACC; 	1 GCCATGGCCTCGTGGGGTTCATCTGG	21 CGTCACCGCGAGGCGCATTTGCCGTT	1 CGCATGCAGGAAGACAATCGAGCTTT	01 ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCT	241 GATTTTICCTTCCTCGGCGGTTCTTTGGGCACGGTCC		121 AACCTCAATCAAGGCTATGCAGAGACCTTGGAGCGC	68 ATAGACTCGGTTTTGGACCCTGACAGCTTCATTT
•	CTGGTCTACGCG 12	CCCCACCGTTTCGGTCATT 114	GAGGAGCTCGGCATCGCAAGC 108	GATCGTGTCC 102 GATCGTGTCC 152	CACGCTTGGGCCGCAGGAG 960	CGCGCATC 90 CGCGCATC 14	TCGTCAAG 84	GITCICGI 78 GITCICGI 12	AGAGGCAACGGATCGT, 72 AGAGGCAACGGATCGT, 12	GAATTGTGTCGCCACTCCAA 66 	GCATGCGCTTCCAGACGGTGTG 60	GGCGCGCAGATA 54	ACGATGGGTGGC 48 ACGATGGGTGGC 98	GCGGCTGTGCAG 42	CTCCCCTGCTTCCGGTGGTGCG 36	TCGGTGCGCATCATGAAGGCG 30	CGGTAGCCGTTATTTTGTCC 24	GAAGCAAGGCCAAATGCGAT 18	AATGAAACTCCCCAATATGAC 6

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Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko i
Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi,
Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com,
Tel:81-44-829-3031, Fax:81-44-813-1651)
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Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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protein"
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db_xref="GI:21323420"
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                                                                                                                                                                                                                                                                                                                                                                                             gene="Cg10654"
note="PF02554:Carbon
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strain="ATCC 13032"
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	CDS	gene	CDS	gene			gene	CDS	gene	CDS	gene
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CDS		;	gene		gene CDS			CDS	gene	CDS	gene

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RSILSIkphttrlriiahsdharlrqsvqehiemcbavasgdlrsagaacrqhlihve
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                                                                                                                                                                                                                                                                                                 GIRAWTNSRKQSKHSQ"
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complement (9094. .9798)
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EC_number="1.1
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Best Local Simi
Matches 1473;
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              GGGGCCCGCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGCTTTGGGCCGCAGGAG
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Qy 1 GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGGCATGGAACACACTTCAGCATTGACGCTC 60	Query Match 100.0%; Score 1473; DB 6; Length 349980; Best Local Similarity 100.0%; Pred. No. 3.4e-293; Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 10 AX127145/c LOCUS DEFINITION Sequence 7061 from Patent EP1108790. ACCESSION AX127145 AX114121 VERSION REYWORDS SOURCE Orynebacterium glutamicum Bacteria; Actinobacteridae; Actinomycetales; Corynebacteriumeae; Corynebacterium. TITLE AUTHORS TOURNAL SOURCE TOURNAL FEATURES SOURCE Source Orynebacterineae; Corynebacteridae; Actinomycetales; Corynebacterineae; Corynebacteridae; Actinomycetales; Corynebacteridae; Actinobacteridae; Actinomycetales; Corynebacteridae; Corynebacterium. TITLE JOURNAL Novel polynucleotides Patent: EP 1108790-A 7061 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP) FEATURES SOURCE Orynebacterium glutamicum AUTHORS Novel polynucleotides 1. 349980 Organism="Orynebacterium glutamicum" /db xref="taxon:1718" /nol_type="genomic DNA" /db xref="taxon:1718" /noce="Seq 1 to long (3.309.400) split in 11, seq 7061 BASE COUNT 79274 a 90638 c 98727 g 81341 t	OY 1441 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1473	Qy 1381 GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGGGGGGGACGCGAC 1440	QY 1321 AGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTC 1380	QY 1261 GACACCAACCACGCGGGAAATCATAGAGCGACAAGGCGTGCAGGCGCACGTTTTA 1320	Qy 1201 GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGGCCCTCGGCCATCCTCTTCCGC 1260	Qy 1141 ATTGGTCAGGGCGTTGGCGGTGGCGATGCTGCCCGGCGGATCTGGTCTACGCG 1200	. QY 1081 TCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCTCCCCACCGTTTCGGTCATT 1140	Qy 1021 ATCATCGACACCTCCGGCGCCCGAATTGTCGCAGGCGGCTGAGGAGCTCGGCATCGCAAGC 1080	QY 961 CTGCGTTTTGCGCGTGGCATTTCGCTGGCGCGAGCTAAACCTGCCGATCGTGTCC 1020

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AP005217.1 GI:23492722
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Direct Submission

AL Submitted (17-MAY-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, Tel:81-3-3481-1933, Fax:81-3-3481-8424) Kawarabayasi, Y is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba, Daraki, 305-8566 Japan

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Corynebacterium efficiens YS-314
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Ikeo,K., Suzuki,M., Mashima,J., Itoh,T., Yamagishi,A., Nishio,Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rrna
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CFDLIDRVGVAAIPVQAPVDKFEQWSSKVRFAFCKQEDTLREAAQRLRAAGSL"
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                                                                                        complement (7180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="rrnA 5S"
/product="58 ribosomal RNA"
/note="CErRNA03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="rrnA_5S"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2042. .2215)
product="hypothetical protein"
                       codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNPPHEHSPWWVY"
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                                                                     note="CE0890"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trans1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="rrnA_23S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MSSQTPNSMPPTYHHHLGDVFADPWVMIHPITTCWWQPHPGSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="CE0886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="rrnA_16S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="rrnA_168"
529. .1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTHASRIMKPCLQGGLVANG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVARLORMLIDALSTAPASTIKEGALGVRMVTRLTRELQVDEQQVARVVSLGVSSGLL
RRGVEDPLPADDGGDY I APTPVADEMLQATLAEQLAHLMRGWMTQTYAAMLVGEADE
KNKP IHLLS PASRRDALPETRAMILGSLTRVGEEDLEADLF FHIPLAASR I PRETIRH
LLEEARWIGAVAGGGVTS PARVLTQAPAGVI PEI ADI AVAVAAPKPVDFF I VQADYV
MVPGFLQPEMQKI IGQLADLESPGLASVYRI SEASLAHAMDLGLTATEI EDFLTQHSA
TGLPQSVAYLLQDI ARRHGTLRGGPALCYLRSDDPALLHSAVEAAGALGIRQI APTVA
VSNASLI EVITALRKAGMQFVAEDALGASLDLAPRPARVPAAEQPRSAGPLDESR IRA
                                                                                                              DLNTVQGIYDAVSGTLAQYGVQVPAEIQAHYNAFIGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMEFPVPAETIGYVHPYTRINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / tränslation="MPCFPF8QIRQTKVTSTAPKLGDIMKKDSPVPTLTGWLEQLDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVAAIRREEVARTGTVSDQPTLAVLQAAVRGQRTVTLGFVDKQGVAVHRTVKPLTVNA
GQVDALDESTGAVHRFMLHRITEVIVD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAHFYSVVSRDTLDTEYAAHRQRFLAEQGYAYRIIDADDLLFPITEKET"
dentity: 52 in 127 aa"
                                             note="CE0895,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPQLIKAGLLSRVDEQTVKLPGVVRRVLEGQEDTAWRVVPVEPSAVPGADDAGIAAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAC17700.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="CE0893, similar
dentity: 50 in 62 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="CE0893,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="CE0892, similar to AE006976-11|AAK45126.1| percent identity: 36 in 741 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                               dentity: 71 in 195 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MGNMANVEKKGYVDPAWPDHDPSEGHVVTELIAPYAGASSPWGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1836. .12036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVVLLALVNTNVDETLPPRWGLAVRTINRLGVHDRKLGERVPSVAVSGRRTIRDQDHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="CE0891,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dentity: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l, similar to AL583924-93 CAC31112.1 percent in 547 aa"
                                  similar to AE006977-4 AAK45135.1 percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to AL583924-91 CAC31110.1 percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX133781-1 | CAC38957.1 | percent
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CDS

1157

1217

24919

24859

24739

24799

1097

25039

1037

25099

24979

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Query Match
Best Local Similarity
Matches 928; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25938
                                                                                                                                                                                                                                                                                                                                                                                                                                       681
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  921
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  GATTGGGCAGGA---TCGCCGCTTCACGCTTGGGCCGCAGGAGCTGCGTTTTGCGCGTCG
                                                        TCGCATCTCGCGGGCGACCACGGTGGCGCTGGCCCGCATCGGGGGGCCGTCCGGTCGTGCT
                                                                                                                                                                                                         CGGGGAGATTATGGAAACGTTGGGGGGCAGACGTCGTCAAGCTTTCTGGTGCGCGTGCTGG
                                                                                                                                                                                                                                                                            GAAACCACGTGGTGCGTGGGAGTCGATCATGATCACCCGGGAACCCGGTCGCCCCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTGGGTCCTCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGTTCGCCATGATGATCTCCATCACCACCGCCGTCTACCGGCACAAGGACGCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGTCTCCCGCTGTTGATCTCGCCGTGCTCGGGTGGCACCCCGGATGCAGGAGGGCACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAACTCCCACTGCTGCTCCCCTGCTTCCGGTGCTGCACGCATGCAGGAAGACAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCGATCGGTGCCGCCACCTCCCGTCGTCTCATCCAGGCCATCCACCGGGCCACGCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGAACGGTGGAGGGCTCCCGCGTGGCGTTCATCGTCTCCGAGTTCGCCTTCCTCGGTGG
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X66112
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Submitted (15-MAY-1992) B.
Forschungszentrum Juelich (
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2 (bases 1 to 3013)
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                                                  /organism="Corynebacterium g
/md_type="genomic DNA"
/strain="ATCC13032"
/db_xref="taxon:1718"
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                                              complete genome.
AE006979 AE000516
AE006979.1 GI:13880475
Mycobacterium tuberculosis Mycobacterium tuberculosis
                                                                                                AE006979 17910 bp Mycobacterium tuberculosis CDC1551,
                                                                                                                 AE006979
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                                                                                                                                                                                                                                                                                               TCCGAATTGGATAACAATCCGGAGAGGGCGGGGACGCGACAGTCGCTTCACACGATTTGAG
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                                                                                                                                                                                                                                                                                                                                                   ATCGTCGCCGAAACCGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCAACGCCCTC 1401
                                                                                                                                                                                                                                                                                                                                                                                                ATCATAGAGCGACAAGGCGTGCAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                    ATCATAGAGCGACAAGGCGTGCAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGG 1341
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PLSGRTLVFIIDLISA"
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterium; Mycobacterium
White, O.,
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O. Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W. Whole genome comparison of Mycobacterium tuberculosis clinical and

Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., DeIcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W. White, O.,

Submitted (25-APR-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA ocation/Qualifiers

organism="Mycobacterium tuberculosis CDC1551" strain="CDC1551" _type="genomic DNA"

/gene="MT0918" 145. .1326 note="identified db_xref="taxon:83331" gene="MT0918" note="clinical strain" by Glimmer2; putative"

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CDS

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TPQQAFAGTFHVNETWSQLDAAYSQAASGLADDLPCBAYCHSLTDPDS ILSARLRDDAF
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GGAVSGIGGHNAAMAVLACLASRRKSP"
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PGWIAHWREMHDEGDSKIGRPRQIYTGYTERDYVTIDAR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGCCGACTCCTATGCGCGGGAGCTGGCCGCCGCTCGGGCGGCCGCCGCGCGGACGAAT 11651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGGCAAAGGCCAAATGCGATGAAT 184
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                                                                                                                                                                                                                                                                                                                                                                                     CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG 11711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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1.ENGSIGAESTWINDCONST
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complement (8122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mmehyhwwlaglaftlgmyltstlmyrpyehqyltykksyrgssa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (9473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (8122. .9531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENSPLGGARLVLRLPGPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7575. .8105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="MT0926"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="similar to PID:2440113; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 312.6; DB 1
Pred. No. 3.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .10183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9531)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 14	8 8 8 8	유 성	ß &	ß 8	8	음 성	유 성	D 4	\$ \$ \$	B 8	8 8	g d	8 B 8	B 8	음 성	8 8 8
IIT 14	1307 CGCACGCACTTITAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAAACCGAGCACTTTG 1366		1187 ATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGG 1246	1127 CCGTTICGGTCATTATIGGTCAGGGCGTTGGCGGTGGCGCGCGTGGCCATGCTGCCGGCGG 1186	1067 TCGGCATCGCAAGCTCGATTGCGCGCACCCTTGTCCAAGCTTATCGACGCTCCCCCCCC	1007 TGCCGATCGTGTCCATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGC 1066	947 TTGGGCCGCAGGAGCTGCGTTTTGCGCGTGGCATTTCGCTGGCGCGAGCTAAACC 1006	10933 GCGGCCAACCCACGGTGGTCCTCGGCCAGCAAAGGGCAGTAGGCGGGGGGAAGCACTG 10874	TITCTGGTGCGCGTGCTGGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCTTGGCGCGCATCG	782 ACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAACGTTGGGGGCAGACGTCGTCAAGC 841	725 CTCCAACAACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTG 781		605 AGGCGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGC 664		485 TGGCCTCGTGGGGTTCATCTGGGCATCTCACCTTTTGCGGAACCCGGCGCGCAGATAAGGTT 544	11470 TGCAAGAAGGCACGGTCGCGTTTCTGCAGATGGTGAAGATCGCTGCGGCCATCCAGCTGC 11411 425 ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA 484
		gene		FEATURES source					COMMENT	TITLE JOURNAL	JOURNAL MEDLINE PUBMED	TITLE		REFERENCE AUTHORS	SOURCE	LOCUS DEFINITION ACCESSION VERSION KEYWORDS
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f M. tuberculosis sequencing at the Sanger Centre are on the World Wide Web.
on the World Wide Web.
on the World Wide Web.
or the World Wide Web.
or the World Wide Web.
or the original cosmid submissions but the old publications are in brackets after the new gene numbers.
iction was based on a Hidden Markov Model of TB genes and in TBparse (Krogh) supplemented with visual inspection mul base preference in codons, especially where there is sent the observed/expected third position G + C.
In some cases we may not have predicted the correct rocdon. Where possible we choose an initiation codon or ttg) which is preceded by an upstream ribosome it sequence (optimally 5-13bp before the initiation if this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-JUN-1998) Submitted on behalf of the Mycobacterium sequencing and mapping teams, Sanger Centre, Wellcome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique acterienne, Institut Pasteur, 28 rue du Docteur Roux, 26 edex 15, France E-mail: parkhill@sanger.ac.uk 1988 this sequence version replaced gi:1314009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rosch,R., Parkhill,J., Garnier,T., Churcher,C.,
yrdon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E.,
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A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
A., Rogers,J., Rutter,S., Taylor,K., Whitehead,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 he biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 37630)
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tuberculosis H37Rv
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neae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             685), 537-544 (1998)
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ion/Qualifiers
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gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="8WISS-PROT:Q10537"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRTGSGALITGYRFDRTARDLHLLLPDPYTFPSNLLIBHPNTDLPGTAVVGGVVSGGR
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3583. .4371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFAGNFTSARLQLGRPAVLVVRCTVLVTVLAIAAAVAGSLAATAIATLITAGSSAIAK
ASLDASLQHDLPEESRASGFGRSESTLQLAWVLGGAVGVLVYTELMVGFTAVSALLIL
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/gene="Rv0875c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3457. .3465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLAQTIVSFRGDSLIPGLGGNRPVMAEQETTRRGAAVAPQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1799. .3445)
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/transT_table=11
/product="hypothetical protein Rv0875c"
/protein id="CAA97382.1"
/db_xref="GI:1314012"
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TDRAADVLSAVLQMIDPPALVGCIAQAIVAGRHEIEDEPAVVVWLASGLAAETFQLDF
                                                                                                                                                                                                                                                                       codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="Rv0877"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv0876c"
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TTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCCGCTCGGTGCGCATCATGAAGGCGATTC 304
                                                                                                                    CGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCCGATT
                                                                                                                                                                    TAGCCGACTCCTATGCGCGGGAGCTGGCCGCCGCTCGGGCGGCCACCGGCGCGCGACGAAT
                                                                                                                                                                                                                  TCAATCAAGGCTATGCAGAGACCTTGGAGCGGCTCGAAGCAAGGCCAAATGCGATGAAT 184
                                                                                                                                                                                                                                                                ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG
                                                                                                                                                                                                                                                                                                            ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC 124
                                                                           CGGTGCAGACCGGTGAGGGACGCGTATTCGGGCCGGCGGGTGGCCGTGGTGAGT
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /HOUGE="RY0880, (MTCY31.08), len: 143, unknown, equivalent to MLCB57_15 Mycobacterium leprae cosmid B57 (143 aa)
033060 HYPOTHETICAL 15.8 KD PROTEIN. FASTA scores: opt:
818 z-score: 980.3 E(): 0; 89.5% identity in 143 aa
0verlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Rv0879c"
/note="Rv0879c,
to MLCB57_14 Mycc
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complement(5989. .6264)
/gene="Rv0879c"
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/gene="Rv0880"
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/product="hypothetical protein
/protein_id="CAA97386.1"
/db_xref="01:1314017"
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/gene="PPE"
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/translation="MSVENSQIREPPPLPPVLLEVWPVIAVGALAWLVAAVAAFVVPG
LASWRPVTVAGLATGLLGTTIFVWQLAAARRGARGAQAGLETYLDPK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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/transl_table=
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/db_xref="GI:1314016"
/db_xref="SWISS-PROT:Q10540"
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                                                                                                                                                                                                                                                                                                                                                                             21.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0879c, (MTCY31.07c), len: 91 unknown, equivalent 14 Mycobacterium leprae 033059 HYPOTHETICAL 9.8 [91 aa), E(): 1.2e-25, 76.9% identity in 91 aa
                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                        Score 312.6; DB 1;
Pred. No. 3.4e-54;
0; Mismatches 589;
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CGGCCGACCTACTGAAGTCGGGGATTGTCGACACCATCGTGCCGGAGTACCCCGACGCCG
                                                                                                                                                                                                                                                                                                    CCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCGCTGGCCATGCTGCCCGCCG
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                                      CGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTG
                                                                                       CGATCGTGTTCCGAGACACTGCTCATGCCGCCGAACTCGCTGCCGCCCAAGGCATCCGGT
                                                                                                                                  CCATCCTCTTCCGCGACACCAACCACGCCGCGAAATCATAGAGCGACAAGGCGTGCAGG
                                                                                                                                                                               ACCGGGTGCTGGCCGCACTCCACGGCTGGCTGGCGCCCTTGCCTCCCGAAGGAGCCAGCG
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Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire Submitted (24-MAR-2003) Garnier 75.74 PARIS cedex 15, France. e-mailitgarnier@pasteur.fr Submitted on behalf of the Mycobacterium bovis sequencing teams, TB Research Group, Veterinary Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone, Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, UK. PT4 Annotation, Genopole, Institut Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France. Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France
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Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,
Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L.,
Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of Mycobacterium Online Publication PNAS 10.1073/pnas.1130426100 ( Microbiology )
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Mycobacterium bovis subsp. bovis AF2122/97
Mycobacterium bovis subsp. bovis AF2122/97
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Mycobacterium bovis subsp.
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                                                                                                                                                                                                                                                                                                                                                        /notee "Mb0912, -, len: 490 aa. Equivalent to Rv0888, le
490 aa, from Mycobacterium tuberculosis strain H37Rv,
(100.0% identity in 490 aa overlap). Probable exported
protein. Equivalent to AAK45157.1 from Mycobacterium
tuberculosis strain CDC1551 (507 aa) but shorter 17 aa.
Contains possible N-terminal signal sequence."
                   complement (2205. .3326)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="Mb0912"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mycobacterium/mol_type="genomic DNA"/strain="AF2122/97"
                                                                                                                                                                                                                                                                                                                codon_start=1/transl_table=
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bovis AF2122/97 complete
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bovis

len:

CDS

CDS gene

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/incus_tay=rmosyle, / len: 882 aa. Equivalent to Rv0890c, /notes_rmb0914c, -, len: 882 aa. Equivalent to Rv0890c, len: 882 aa, from Mycobacterium tuberculosis strain H37Rv, (99.9% identity in 882 aa overlap). Probable transcriptional regulatory protein, LuxR family, highly similar (but shorter 238 aa in N-terminus) to NP 302202.1|NC 002677 possible transcriptional regulator from Mycobacterium leptrae (1106 aa). Also highly similar (generally in part) to others e.g. T50568 probable multi-domain regulatory protein from Streptomyces coelicolor (1334 aa); p10957|NARL ECOLI nitrate/nitrite response regulatory protein from Escherichia coli (216 aa), FASTA scores: opt: 193, E(): 6e-06, (37.4% identity in 99 aa overlap); etc. Also highly similar to others from Mycobacterium tuberculosis e.g. MTCV02BL0 22, MTV008 44, MTV036 21, and MTCY31_24. Contains p80017 Arp/GTP-binding site motif A (P-loop), P806622 Bacterial regulatory proteins, luxR family signature, and probable helix-turn helix motif from aa 836 to 857 (Score 1559, +4.50 SD).
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CAB95899.1|AL359988 putative citrate synthase from Streptomyces coelicolor (387 aa); P39119|CISY BACSU citrate synthase II from Bacillus subtilis (366 aa), FASTA scores: opt: 586, E(): 5.8e-30, (33.8% identity in 367 aa overlap); etc. Also similar to Rv0896|MTCY31.24 from Mycobacterium tuberculosis (29.2% identity in 274 aa overlap) and Rv1131. Contains PS00480 Citrate synthase signature. BELONGS TO THE CITRATE SYNTHASE FAMILY."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="PROBABLE CITRATE SYNTHASE II CITA"
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                                                                                                                                                                                                                                                                                                                         NAAAVGEI CRRLDGI PLAI EFAAARVRSMS PLEI ADGLDDCFRLLAGGVRGAVQRQQT
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complement(3413. .60)
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dvptkvlglytqaqvlaycgasaahaiagaciaāatelggvyqgigyaamtyaalaag
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complement(2205. .3326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein_id="CAD93775.1"
db_xref="GI:31617666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN PROBABLY LUXR-FAMILY)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus_tag="Mb0913c"
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TCAATCAAGGCTATGCAGAGACCTTGGAGCGGCTCGAAGCAAGGCCAAATGCGATGAAT 184 ACGCGGTGCTAGACCGGGGATCTTTCGTCAGCTGGGATAGCGAGCCGCTGGCGGTGCCGG 21555 ACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACC 124 Best Local Similarity Matches 717; Conserv

Conservative

0

21.2%;

Score 312.6; 1 Pred. No. 2.6e 0; Mismatches

2.6e-54; DB 1;

Indels

Gaps

u '

Length 327650;

Query Match

gene

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/note="wb0916, -, len: 495 aa. Equivalent to Rv0892, len: 495 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 495 aa overlap). Probable monooxygenase (EC 1.14.-.), highly similar to others e.g. NP 250787.1 NC 002516 probable flavin-binding monooxygenase from Pseudomonas aeruginosa (491 aa); CAB59668.1 AL132674 monooxygenase from Streptomyces coelicolor (519 aa); P12015 (CYMO ACIS cyclohexanone monooxygenase from Acinetobacter sp. (542 aa), FASTA scores: opt: 489, E(): 6.8e-26, (30.3% identity in 492 aa overlap); etc. Also highly similar to Rv0565c, Rv3854c, Rv3083, etc from Mycobacterium tuberculosis. Has hydrophobic stretch at N-terminus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (99.6% identity in 285 as overlap). Possible transcriptional regulator, highly similar in N-terminus to NP 302202.1 |NC 002677 possible transcriptional regulator from Mycobacterium leprae (1106 as). Also highly similar to several Mycobacterium tuberculosis putative transcriptional regulators e.g. Q1102 |MTCY02B10 22 PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN (1159 as), PASTA scores: opt: 702, E(): 8.3e-40, (50.6% identity in 247 as overlap); MTV036_21; MTV008_44; MTCY02B10_23. Also shows similarity with several adenylate cyclases and hydrolases from other organisms."
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                                     TPDYEPMCKRLVMSGGFYRAIQRDDVELVTAGIDHVEHRGIVTDDGVLHEVDVIVLAT
GFDSHAFFRPMQLTGRDGIRIDDVMQDGPHAHQTVAIPGFPNFFMMLGPHSPVGNFPL
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GRLPADAWLVDLGRHPLRGLPRPEWVMQLCHPDIREKFPPLRTAKSSPTSILPAQFTT
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EAIAYAQRGRGERKRPARGWGSLTPTERDVVRLVSEGLSNKDIAKRLFVSPRTVQTHL
THVVAKLGLASRVQLVDEAARRGSPS"
TAVAESQAEHIVQWIKRWRHGEFDTMEPKSAATEAYNTVLRAAMPNTVWTTGCDSWYI
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/318. .8805
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Search completed: November 13, 2003, 00:10:39 Job time: 5538.03 secs

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Maximum DB
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Perfect score:
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             312.6
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100.0 1473
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Match Length
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                                                         AAH51981
                                                                                                           AAH65894
AAC82733
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  C glutamicum codin
C. glutamicum accD
Corynebacterium gl
C. glutamicum accD
C glutamicum codin
Mycobacterium tube
Mycobacterium tube
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Genomic fragment #	AAF28528	22	28626	5.9	87.4	4 5	
Magnetospirullum s	AAT90220	18	954	5.9	87.4	44	
Listeria monocytog	ABA03041	24	10		88	43	Ω
Genomic sequence o	ABA90521	24	58	•	91	42	
DNA sequence upstr	ABK37820	24	1001	٠	92.8	41	
Haemophilus influe	AAF91440	22	1001	٠		40	
2CFE 67 coding seq	AAH90875	22	891	6.3	93	39	
Streptococcus pneu	AAS55630	23	867	٠		38	
Listeria innocua D	ABQ69245	24	3011208		•	37	O
Listeria innocua c	ABQ67195	24	495269	٠	•	36	
Streptococcus poly	ABN71527	24	2155561	6.4	94.2	35	
Streptococcus poly	ABN68650		873	٠	•	34	
Streptococcus pneu	ABS56454	25	2162598	٠	•	ω u	
Haemophilus influe	AAT42063	17	1830121		•	32	
	AAV52140	19	19702		•	31	a
S. pneumoniae deri	AAZ96348	19	1595	٠	•	30	O
Haemophilus influe	AAS53478	23	891		•	29	
	AAH90763	22	867		•	28	
S. pneumoniae type	ABX06060		864		96.2	27	
Bacillus clausii g	ABK78240		654		96.8	26	
Streptococcus pneu	AAS55883	23	867	6.6	97.8	25	
nove	AAS89710		3318	•	99.8	24	
\ encoding nov	AAS88487		3318	•	w	23	
Ω	AAS52496		915	•	102.8	22	
typhi	AAS56217		993	7.3	108	21	
	ABZ75344		23673	•	108.6	20	ი
N. meningitidis B	AAA81490		1437668	8.1	118.6	19	
Neisseria meningit	AAF21608	21	349980	8.1	118.6	18	
H. pylori GHPO 451	AAX14153	19	1053	8.1	119.2	17	
Helicobacter pylor	ABX65721	24	877	8.1	119.2	16	
Helicobacter pylor	AAS53651	23	870	٠	119.2	15	
Helicobacter pylor	ABX65750	24	676		119.2	14	
	ABS99190	24	6021	•	121	13	
	AAX13395	20	6021		121	12	
terococcus f	AAS53191	23	867	8.2	121	11	
Œ	390	25	876	8.3		10	
Pseudomonas aerugi	AAS54163	23	873	8.3	122.8	9	

ALIGNMENTS

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RESULT 1
AAH65894
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07-APR-2000;
03-AUG-2000;
WPI; 2001-376931/40
                                                                                 Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C glutamicum coding sequence fragment SEQ ID NO: 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2001
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                                                                                                                                                                                                                     (КУОМ ) КУОМА НАККО КОБУО КК.
                                                                                                                                                                                                                                                                                                   99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                             Mizoguchi H,
Senoh A, Ike
                                                                                 H, Ando S, Hayashi M, Ikeda M, Ozaki A;
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly I-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1473 BP; 275 A; 414 C; 456 G; 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                          541
                                              601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGGATTCCGGTAGCCGTTATTTTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCTCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCAAGGCCAAATGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC
              CAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTTGTCGCCACTCCAA
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                                                                                                                                                              GCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCAGATA
                                                                                                                                                                                                                          CGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGC
                                                                                                                                                                                                                                                                      CGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAG
                                                                                                                                                                                                                                                                                                                                     ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCG
                                                                                                                                                                                                                                                                                                                                                       ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGCTCCCCCTGCTTCCGGTGGTGCG
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C. glutamicum accDA DNA #2.	15-MAR-2001 (first entry)	AAC82733;	SULT 2 C82733 AAC82733 standard; DNA; 1473 BP.	1441 AGTCGCTTCACACGATTTGAGCGTTTAGCGCAG 1473 	1381 GGCACAATCAGCAACGCCCTCTCCCGAATTGGATAACAATCCCGGAGAGGGC	1321 AGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGA	1261 GACACCAACCACGCGGGGAAATCATAGAGCGACAAGGCGTGCAGGCGCACGTTTTA	1201 GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCCGGCCATCCTCTTCCGC	1141 ATTGGTCAGGGCGTTGGCGGTGGCGCGCTGGCCATGCTGCCCGCCGATCTGGTCTACGCG	1081 TCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCTCCCCACCGTTTCCGGTCATT	1021 ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGCTCGGC	961 CTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGCGAGCTAAACCTGCC	901 GGGGGCCGGCCCGTGGTGCTGATTGGGCAGGATCGCCGCTTCACGCTTGGGCCGCAGGAG	841 CTTTCTGGTGCGCGTGCTGGCGCATTGAGCCCGGCTGTGCGCGTTGCCCCTGGCGCGCAT	781 GACCCGCAGAGGCCTGGAATCGGGGAGATTATGGAAAACGTTGGGGGCAGACGTCGTCAAG	721 TTTCTCCAACAACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCG	661 TTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGT
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L-amino acid; accDA; coryneform microorganism; L-lysine; animal feed; medicine; pharmaceutical industry; ds.

Corynebacterium glutamicum.

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EP1055725-A2

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Query Match
Best Local Similarity
Matches 1473; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a fully defined 491 as sequence; (2) coryneform microorganisms transformed with one or more copies of (1); (3) the shuttle vector pZlaccDA contained in Corynebacterium glutamicum DSM 12785; and (4) a process for producing L-amino acids, comprising culturing a coryneform bacterium that overexpresses the accDA gene. Coryneform bacteriam that overexpresses the accDA gene coryneform bacteria transformed with (1) so that they overexpress the accDA gene useful for producing L-amino acids, especially L-lysine, which are useful in animal feeds, in human medicine and in the pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel cloned Corynebacterium glutamicum DNA (I), replicable in coryneform microorganisms coding for an accDA gene. The invention also describes (I) a polypeptide derived from (I) having a fully defined 491 as sequence; (2) coryneform microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloned Corynebacterium glutamicum accDA gene useful transformed coryneform bacteria producing increased acids, especially L-lysine -
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P-PSDB; AAB45789.
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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine
                                                                                        Corynebacterium glutamicum nucleic acids encoding membrane con and membrane transport proteins or their portions, useful for identifying C. glutamicum or related bacteria, and as markers transformation -
                                                                                                                                                         WPI; 2001-071486/08.
P-PSDB; AAB76522.
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chemicals, for modulating fine chemical production in C. glutamicum related bacteria (e.g. Brevibacterium lactofermentum), the typing on identification of C. glutamicum or related bacteria, as reference po for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in a in C. s 'n or points ဝူ an

1473; No. 0; 358 DВ Ţ, 0 22; other; Length

GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC GATTTTTCCTTCGCCGCGGTTCTTTGGGCACGGTCGCGTCGCGCATCATGAAGGCG GATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCG GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCC GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCC AACCTCAATCAAGGCTATGCAGAGACCTTGGAGCGGGCTCGAAGCAAGGCCAAATGCGAT ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCCAATATGAC ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCCTGCTTCCGGTGGTGCG ATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCG ATAGACTCGGTTTTGGACCCTGACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGAC GTGGAGAAGCGTTTTCCGACTATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTC AACCTCAATCAAGGCTATGCAGAGACCTTGGAGCGGCTCGAAGCAAGGCCAAATGCGAT Mismatches 0; Indels o ;-379 300 139 420 439 360 319 240 259 199 120 60

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GCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAGATA CGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCCACGATGGGTGGC GCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATA

GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG GGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTG

CAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAA

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TTTTCTCCAACAACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGT TTTTCTCCAACAACTCCTGGCGTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGT TTGCGTGCAGCGGTGGCAAAAACCCTCAAGGTTATTCAGCCGGT 799

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901 GGGGGCCGGCCGGTGCTTCATTGGGCAGGATTCACCGTTCACGCTTGGGCCGCAACTTCACGCTTCACGCTTCACGCTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGGGCCGCAACTTCACGTTTGCGCAACTTTGGGCCGAACTTTACCGTTGCGAACTTGGGAACTTTGGGAACTTTGGGAACTTTTGGGAACTTTTGGGAACTTTTGGGAACTTTTGGGAACTTTTGGAACATTTGGAACATTGGAACTTATGGAACATTGGAACTTATGGAACATTGGAACTTATGGAACATTGGAACTTATGGAACATTGGAACTTGGAACTTGGAACTTTTGGAACATTGGAACTTATGGAACATTGGAACTTTTGGAACATTGGAACTTATGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACATTGGAACAAACCAACTTTTGTTGAAGAAATTCTTTTATGAACAAACCAACTTTTGGAACAAATTGGAAAAATCAAAACCAAAATCAAAACCAAAATCAAAACCAAAATCAAAAACCAAAAACAAAATCAAAACCAAAAATCAAAACCAAAATCAAAACCAAAAATCAAAACCAAATTAAACAAATCAAACCAAATTAAACCAAATTAAACCAAATTAAACCAAATTAAACCAAATTAAACCAACTTTTTGGAAAATTCAAACCAATTTAACCACAAATTAAACCAACTTTTTGGAAATTTGGAAAATCAAATCAAACCAAATTAAACCAATTTAAACCAATTTAACCACAAATTAAACCAAATTAAACCAATTTAACCACAAATTTAACCACAAATTAAAACCAATTTAAACCACTTTTTAACCACAAATCAAACCAATTTAAACCACTTTTTAACCACAAATTAAACAATTTGGAAATTTAACACCATTTTAACCACAAATCAAACCAAATTTAAACAATTTTAACACCAATTTAACCACAAATTTAACCACAATTTAACCACAAATTTAACCACTATTTAACCACAAATTTAACCACAAATCAAACCAAATTTAAACAATTTAAAATTCGAAAATCAAAATCAAATTTAAAATT	

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L-amino acid; accDA; coryneform microorganism; L-lysine; animal feed; medicine; pharmaceutical industry; ds.
Cloned Corynebacterium glutamicum accDA gene useful for producing
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This invention describes a novel cloned Corynebacterium glutamicum DNA
CC (I), replicable in coryneform microorganisms coding for an accDA gene
CC (I), replicable in coryneform microorganisms coding for an accDA gene
CC the invention also describes (1) a polypeptide derived from (I) having
CC tally defined 491 as sequence; (2) coryneform microorganisms
CC transformed with one or more copies of (I), the shuttle vector
CC transformed in Corynebacterium glutamicum psm 12785; and a

CC transformed with (COrynebacterium glutamicum psm 12785; and a

CC transformed with (COrynebacterium glutamicum psm 12785; and a

CC (4) a process for producing 1-amino acids, comprising culturing
CC (4) a process for producing verexpress the accDA gene are
CC (4) a process for producing 1-amino acids, especially 1-lysine, which are
CC useful for producing 1-amino acids, especially in the pharmaceutical
CC useful in animal feeds, in human medicine and in the pharmaceutical

CC useful in animal feeds, in human medicine and in the pharmaceutical
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EP1055725-A2 29-NOV-2000.

10-MAY-2000; 2000EP-0109842.

99DE-1024365.

(DEGS) 27-MAY-1999;

DEGUSSA-HUELS AG. FORSCHUNGSZENTRUM JUELICH GMBH.

<u> Eikmanns</u>

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Sahm H,

Moeckel

Tilg Y, Eggeling L, WPI; 2001-042411/06. P-PSDB; AAB45789.

Corynebacterium glutamicum.

AAC82732 standard; DNA; 2123 BP.

AAC82732;

15-MAR-2001

(first entry)

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XX AAH685
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DE C glut
XX Coryne
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KW Organi
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07-APR-2000;
03-AUG-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Best Local Similarity 54.0%;
Matches 717; Conservative
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12-NOV-1999;
12-NOV-1999;
01-FEB-2000;
                                                        Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                       WPI; 2001
P-PSDB; /
Disclosure; Page 74; 207pp; English
                                                                                                                                                                                                 Eisenberg
                                                                                                                                                                                                                                                                                                                                                          13-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis potential drug target
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DB; AAG81130.
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This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of

Sequence 1488 BP; 220 A; 509 C; 524 G; 235 T; 0 other;

Length

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evaluating strain variation of Mycobacterium tuberculosis, compredetermining the nucleotide sequence of the strain at positions i genome corresponding to positions where M. tuberculosis strains 1551 and H37Rv differ
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                                                                                                            CGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTG
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                                                                                                                                                                                                                                             genes, their use in the discovery of movel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The clivention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen cfor homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

CC wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.
   Query Match 8.3%;
Best Local Similarity 52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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23-MAY-2000;
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                                                                                            Sequence 873 BP; 152 A; 285 C; 276 G; 160 T; 0 other;
                                                                                                                                                                                            of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Seq ID No 7800; 511pp; English
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P-PSDB; AAU36304.
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Yamamoto RT,
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16-FEB-2001;
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23-OCT-2000;
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; 2000US-242578P.
; 2000US-253625P.
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Xu HH;
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The present invention relates to proteins from Neisseria gonorrhoeae Also disclosed are the nucleic acid molecules encoding the proteins antibodies that specifically bind to the proteins. The composition
                                        Disclosure; Page 377; 815pp; English.
                                                             New protein
medicament f
                                                                                                                                                               12-FEB-2001; 2001GB-0003424
                                                                                                                                                                                  12-FEB-2002; 2002WO-IB02069
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                                                                                                                                                                                                                                          Neisseria gonorrhoeae
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                                                                                                                      Pizza M,
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Best Local Similarity
Matches 280; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoes infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 876 BP; 183 A; 216 C; 272 G; 205 T; 0 other;
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                                                                J.T.G
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ATG
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                                                                                                                       CAACGCGCCGAGTTTCTGCTGGAAAAAAGGCGCGATCGACCAGATTGTCGACCGCCGCGAT
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Pred. No. 2.2e-24;
0; Mismatches 263
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RESULT 11
AAS53191
ID AAS53
XX AS53
XX AS53
XX AS53
XX AS53
XX AS55
DT .13-FE
XX Antis
XX ANT
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AAS53191 standard; DNA; 867 ₽₽

AAS53191;

.13-FEB-2002 (first entry)

Enterococcus faecalis DNA for cellular proliferation protein #619

Antisense; d antibiotic; ds; prokaryotic cellular proliferation
; antibacterial; drug design. gene;

Enterococcus faecalis

WO200170955-A2

27-SEP-2001

and

21-MAR-2001; 2001WO-US09180.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antiblotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; Seq ID No 6828; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT
                                  GGTGTTACCGCAAGTTTTGCGATGGATGGCGATATTATTTTGGCAGAGCCTCAGAGTTTA
                                                                   ġĠĊĠĊĊĄTĠĠĊĊŢĊĠŢĠĠĠĠŢŢĊĂŢĊŢĠĠĠĊĄŢĊŢĊĄĊŢŢŢŢĠĊĠĠĄĄĊĊĊĠĠĊĠĊĠĊŊĠ
                                                                                                       CAACGGCATAACAAAGCAGGCTTGCTGTATCTTACGGTATTGACTGATCCAACGACTGGC
                                                                                                                                        CAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGT
                                                                                                                                                                          GCCCGTATGCAAGAAGGAATTTTTTCATTGATGCAAATGGCGAAAATTTCGGCCGCTTTG
                                                                                                                                                                                                           GCGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTG
                                                                                                                                                                                                                                               TTGTTTGAGCGGGCGACAGAAAAGCATTTACCAGTAGTGATTTTCACTGCATCTGGTGGT
                                                                                                                                                                                                                                                                  GCGATTCACCGCGCCACAGAGCTGAAAACTCCCACTGCTGCTGCTCCCCCTGCTTCCGGTGGT
                                                                                                                                                                                                                                                                                                                   ATGGACGCTAATTTTATCATGGGCAGTATGGGAACGATTGTTGGTGAAAAATCACACGC
                                                                                                                                                                                                                                                                                                                                                   TCCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGCTCGCGTCGGTGCGCATCATGAAG
                                                                                                                                                                                                                                                                                                                                                                                      GATGAAGCTGTCTTAACGGGAGAAGCAACAATTGAAGGACAAGCTGTTGCAATTGGAATC
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2000US-206848P;
; 2000US-207727P;
; 2000US-242578P;
2000US-257931P;
; 2000US-257931P;
; 2001US-269308P.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 A; 145 C; 209 G; 247 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.2%;
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Pred. No. 4.7e-24;
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178 GATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTG 237

Query Match Best Local S Matches 259

Similarity

8.2%;

259;

Conservative

0;

Score 121; DB 20; Pred. No. 1.1e-23; 0; Mismatches 230;

Length 6021; Indels

0;

Gaps

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RESULT 12
AAX13395
ID AAX13
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06-MAY-1997;
16-MAY-1997;
                                      progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                         A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococal infection in a animal and monitoring
                                                                                                                                                                                                                                                                                     New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fouse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1999
Sequence 6021 BP; 1920 A; 1007 C; 1415
                                                                                                                                                                                                                                              Claim 1; Page 1691-1694; 2084pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis; contig;
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         computer readable medium;
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G; 1673 T; 6 other;
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RESULT 13
ABS99190
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           Computer readable medium having recorded on it a Enterococcus nucleotide sequence useful for detecting diseases related to Enterococcus infections in animals
                                                                                                                                                            04-MAY-1998;
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                                                                                                                                                                                                                                                             Enterococcus faecalis.
                                                                                                                                                                                                                                                                                            Computer readable medium; Enterococcus faecalis; microbe; growth; pathogenicity; vaccine; resistance; Enterococcal infection; commercial; therapeutic; industrial; fermenting; sugar source; metabolite; vaccine; biochip technology; antibacterial; modulator of nucleic acid expression
                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis contig sequence #458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animals, and for detecting E.faecalis using blochip technology. The present nucleic acid sequence represents an Enterococcus faecalis cor DNA sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at http.sequdata.uspto.gov.
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Pred. No. 1.1e-23
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Protein-protein interaction; ulcer; selected SID; gene; ds.

interacting

DNA #349. domain;

Helicobacter pylori selected interacting domain (SID)

(first

entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This sequence encodes a selected interacting domain (SID), identified via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 676 BP; 183 A; 119 C; 190 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 172; 642pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ulcers in mammals
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CACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGGTGAAAAACTGGTGT
                        CATTATCGCAGAGCCAGGGCGATGATAGGCTTTGCGGGGCCTAGGGTGATTAAGCAAAC
                                                 CACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAAC
                                                                             GCTCTTAAGCGATCCCACTTATGGGGGCGTTAGCGCATCTTTTTGCTTTTTTAGGGGATCT
                                                                                              GTATTTGCGCAATCCCACGATGGGTGGGCGCCATGGCCTCGTGGGGTTCATCTGGGCATCT
                                                                                                                                  GATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGT
                                                                                                                                                                                    ATTGATTGTTTCAGCGAGTGGGGGGGCTAGGATGCAAGAATCCACTTATTCGCTCATGCA
                                                                                                                                                                                                              GCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGGAAGACAATCGAGCTTTTGTCAT
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                                                                                               The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antiblotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an CC essential prokaryotic cellular proliferation protein. CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                     Sequence
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23-MAY-2000;
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antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides for the identification and development ibiotics, comprise sequences of antisense nucleic acids
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Query Match

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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                            Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J., R
,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B., Gardner,M.J.
and Collins,F.H.
                                                                                                                                        Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                           12655398
Other_GSSs: AG-ND-133C23.TR
                                                      Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the malaria mosquito Anopheles gambiae Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                                 Anopheles.
1 (bases 1 to 488)
                                                                                                                                                                                                 , genomic survey sequence. BH379574
                                                                                                                                                                                                                 BH379574 488 bp DNA linear GSS 10-DEC-2001 AG-ND-133C23.TF ND-TAM Anopheles gambiae genomic clone AG-ND-133C23
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BH925341 odi46f02.
BZ553868 pacs1-60
BZ579921 msh2 686.
BI725648 1031080B1
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CB081454 hk51h06.g
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BH77989 GOHQB36TF
BH477984 BOHQD36TF
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7 EST531247
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Lefebvre

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ACCESSION
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235; Conserv
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
                                                                                            1112113F06.y1 C. reir
(normalized), Lambda
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Tel: 301 838 0208
Fax: 301 838 3543
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/mol_type="genomic DNA"
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/clone="AS-ND-133C23"
/clone="AS-ND-13AM"
/clone="Vector: pECBAC1; Site 1: Hi
/note="Vector: DECBAC1; Site 1: Hi
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Tel: 919 613 8159
Fax: 919 613 8177
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1 (bases 1 to 707)

1 (bases 1 to 707)

1 (consuman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lef P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation Vascular Plants. Project: 1112
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: chauser@duke.edu.
Location/Qualifiers
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CTCGGCCATCCTCTCCGCGACACCAACCACGCCGCGGAAATCATAGAGCGACAAGGCGT 1301
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                                                                                                                                                                                                                              GGAGCTGGGCCAGGGCGAGGCCATTGCCGTGAACCTGCGTGAGATGTTCGGCCTGCGTGT 465
                                                                               CGCCAACCGCAACCTGATCATGGAGAACGCGGTCTACTACGTGGCCTCGCCCGAGGCCTG 585
                                                                                                                             CGCCGATCTGGTCTACGCGGCCGAAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGC 1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XhoI; Gamete library was constructed by Hui Zhao, Min Lu, Jeffrey McDermott, William J. Snell and John Davies. Strain 21gr cells (CC-1690; mating type plus) and strain 6145c cells (CC-1691; mating type minus) that had been growing on a light-dark cycle (13:11 L/D) in R-medium (Sager and Granick) were separately transfered into nitrogen-free medium at 8 hours into the light period. Polya mRNA was purified from each sample every 2 hours for the next 18 hours. The mRNA was pooled and used for CDNA synthesis. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites, pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Stratagene) phage. The library was normalized usin method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
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/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2
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/mol_type="mRNA"
/strain="21gr (CC-1690 wild type mt+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:3055"
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Pred. No. 2.5e-12;
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707; 0

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345

6145c

(CC-1691

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/clone llb="USSU" SBluescript SK-; Site_1: EcoRI; Site_2: /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested from	Db 73 GTTCAAACAGGCACAGGTCAAGTAAATGGTATTCCTGTAGCAATAGGTATTATGGATTTT 132
/tissue_type="immature seeds" /dev_stage="Immature seeds, 11 to 19 days after pollination"	13 AATGATTATCAAAATCGTCTTGATTCTTATCAAGACCAGAACCGGATTACTGGATGCG
/db_xref="taxon:3880" /clone="pGESD15E20"	: ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
/organism="Medicago truncatula" /mol_type="mRNA" /cultivar="A17"	Unery Match 5.7%; Score 84.2; DB 9; Length 604; Best Local Similarity 48.88; Pred. No. 8.3e-12; Matches 258; Conservative 0; Mismatches 268; Indels 3; Gaps 1;
info	helper phage and propagated in XLOLR cells.
rdx: /13-/98-/078 Email: mgrusak@bcm.tmc.edu B398601e TTCD recompce name. MTDn72/TV	Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zan phage weing Fy-actist
1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713-798-7044	g z
	/clone_lib="MHAM" /note="Vector: pBluescript SX-; Site_1: EcoRI; Site_2: /hotnux was recovered from policy - Translated but from
TITLE ESTs from developing reproductive tissues of Medicago truncatula JOURNAL Unpublished	made from a mixture of RNA from each of these stages." /lab host="E. coli strain XLOIR"
REFERENCE 1 (bases 1 to 773) AUTHORS Grusak, M.A., Samar, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho	vith Glomus versiformed 10, 17, 22, 31 and 38 training The library
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.	/db xref="taxon:119092" /clone="MHAM-7I10"
Chermatonhuta. Macmolionhuta. andicottledona. core endicots. rosida	/mol type="mRNA" /cullivar="Medicago truncatula genotype A17"
Medicago	707
	FEATURES Location/Qualifiers
LOCUS BI311746 773 bp mRNA linear EST 20-UUL-2001 DEFINITION EST5313496 GESD Medicago truncatula cDNA clone pGESD15E20 5' end, mRNA sequence. ACCRSSION RT311746	Other name: MAAM-7b-E05; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'. Seq primer: T3.
T 4	•
Db 493 TCGGCTGAATTTTTATTCGAAAAGGGTGCATTTGATTCACTCGTACCAC 541	The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73401 Tel. SRO.231-SRIO
Qy 604 CAGGCGGAGAATTTGGTGAAAACTGGTGTGATTGATGGAATTGGTGTCGC 652	JOURNAL Unpublished COMMENT Contact: Harrison M.J. Plant Biology Division
	ESTs from roots of Medicago truncatula after coloniza Glomus versiforme
	Harrison, M.J., Bowman, C.L., Ci
Qy 484 ATGGCCTCGTGGGGTTCATCTGGGGATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGT 543	NISM Medicago truncatula/Glomus versiforme Eukaryota; mixed EST libraries.
313 CAAATCAATCAAAAGTTATTCTATGTACCGATACTTACATCTCCTACTACTGGGGGTA	AW584783.1 GI:7261837 EST. Medicado truncatula/Glomus versiforme mixed EST
427 CGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCC	library cDNA clone MHAM-7110, mRNA sequence. ON AW584783
Oy 367 CAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCAC 426	AW584783 LOCUS AW584783 604 bp mRNA linear EST 07-SEP-2000 DEFINITION N210917e MHAM Medicago truncatula/Glomus versiforme mixed EST
Db 193 TATGCTACCAATCAACGTTTACCTCTTATTATAGTATGTGCGTCTGGAGGAGGAGCGCGTATG 252	RESULT 3
Qy 307 CGCGCCACAGAGCTGAAACTCCCACTGCTCCCCCTGCTTCCGGTGGTGCGCGCATG 366	Db 646 CACCICGGCGAAGCIGGTGAAGTICGGCGTCAIGGACCATCGIGCCGA 696
133 GAGTTTATGGGAGGTAGGGGATCCGTAGTGGGTGAGAAAATCACTCGGTTGATTGA	Qy 1302 GCAGGCGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGA 1352
Qy 247 TCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTGGGTGCGCATCATGAAGGCGATTCAC 306	Db 586 CGCCGCCATCCTGTGGAAGAGCCGCTCTGCCGCCGGCGAGGCCACTGAGGCCCTGCGCAT: 645

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                                                                                                                                                                                                                                                                       pacs1-60 1377.sl pacs1-60 Pseudomonas aeruginosa pacs1-60_1377, genomic survey sequence.
1 (bases 1 to 163)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.
Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                            BZ548722.1
                                                                                                                                                                                                                Pseudomonas aeruginosa
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Pred. No. 2.5e-11;
0; Mismatches 269;
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University of Washington
Box 352145, Seattle, WA 98
Tel: 2062216954
Fax: 2066857244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity 49.8
206; Conservative
                                                                                                     Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                Grusak, M.A., Samac, D.A., ,J. and Fraser, C.M.
                                                                                                                                                                                                                             mRNA sequence.
HI310727
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                Unpublished
                               ESTs from developing reproductive
                                                                                                  Medicago.
                                                                                                                                                                           Medicago truncatula (barrel medic)
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/clone_lib="pacs1-60"
/note="clinical isolate 1-60
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/strain="1-60"
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Pred. No. 6.6e-11;
0; Mismatches 208;
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                                                               Town, C.D.,
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                                 of Medicago truncatula
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BASE COUNT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR sequence name: MTPAL60TK
More information is available at:
Seq primer: SKmod (CTA 9AA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1100 Bates Street, Houston, Tel: 713-798-7044 Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA/ARS Children's Nutrition Research Center Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B397582e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                           TATGCTACCAATCAACGTTTACCTCTTATTATAGTATGTGCGTCTGGAGGAGCGCGTATG
                                    TTCCTGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAG 603
                                                                                                                     ATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGT
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                                                                                                                                                                                                                                          CAAGAAGGAAGTTTGAGCTTAATGCAAATGGCTAAAATTTCTGCTTCTTTATATAATTAT
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TTTGCAGGTAAAAGAGTAATTGAAGAAACGTTGAAGATCGAAGTGCCCGAAGGTATACAA
                                                                                                                                                           CAAATCAATCAAAAGTTATTCTATGTACCGATACTTACATCTCCTACTACTGGGGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+enriched RNA. The cDNA was directionally ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phage using | XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vertor: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="immature seeds"
/dev_stage="Immature seeds, 1
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Pred. No.
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gAT CC).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                        235;
                                                                                                              181 GAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGTCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543
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                                       241 GATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCG 300
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosid
spermatophyta; Magnollophyta; eudicotyledons; Trifolieae;
jeurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR sequence name: MTPBX17TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1100 Bates Street, Houston,
Tel: 713 798 7044
Fax: 713 798 7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research
Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheung, F. and Fraser, C.M. More ESTs from developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grusak, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST644115 GESD Medicago truncatula cDNA clone GESD-29C10, mRNA
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GATTTTGAGTTTATGGGAGGTAGTATGGGATCCGTAGTGGGTGAGAAAATCACTCGGTTG 121
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                                                                                   GATGCGGTTCAAACAGGCACAGGTCAAGTAAATGGTATTCCTGTAGCAATAGGTATTATG 61
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                                                                                                                                                                                                                                                                                         171
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                    /note=Tvector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propogated in
XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Immature seeds, 11 to 19
pollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Medicago truncatula"
|mol_type="mRNA"
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                                                                                                                                                                                               5.48;
49.58;
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                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                  129 g
                                                                                                                                                                                               Score 79.8;
Pred. No. 1.
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                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                 1.3e-10;
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                                                                                                                                                                                                                                                                              Email: mjharrison@noble.org
Noble EST name: N380393e TIGR sequence name: MTDBW35TK
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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EST486683 MHAM Medicago truncatula/Glomus versiforme
library cDNA clone pMHAM-20E21 5' end, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                           Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                     2510 Sam Noble Parkway, Ardmore,
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          /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhOI, cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from
                                                                                                                 tissue_type="roots colonized with Glomus versiforme, dev stage="Roots harvested at 10, 17, 22, 31 and 38 post-inoculation with Glomus versiforme. The library made from a mixture of RNA from each of these stages.
                                                                                                        /lab
                                                                                                                                                                                            /cultivar="Medicago truncatula
/db xref="taxon:119092"
                                                                                                                                                                                                                          /mol
                                                                                                                                                                                                                                      /organism="Medicago truncatula/Glomus
                                                                                                                                                                           /clone="pMHAM-20E21"
                                                                                                                                                                                                                       _type="mRNA"
                                                                                       host="E. coli strain XLOLR"
ne_lib="MHAM"
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and packaged using Gigapack III Gold packaging
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                                                                                       Tel: 2062216954
Fax: 2066857244
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112 c 151 g 265 t
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1042 bp DNA linear pacs2-164_3167.y3 pacs2-164 Pseudomonas aeruginosa pacs2-164_3167, genomic survey sequence BZ561247 Whole-Genome-Sequence variation Psedomonas aeruginosa library J. Bacteriol, (2002) In press University of Washington Box 352145, Seattle, WA Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V. Contact: Chris K. Raymond Pseudomonadaceae; Pseudomonas. Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonas aeruginosa Pseudomonas aeruginosa BZ561247.1 GI:27180878 (bases 1 to 1042) craymond@u.washington. Location/Qualifiers /mol_type="genomic organism="Pseudomonas .1042 98105-2145, aeruginosa' among multiple USA Sims, E. isolates Pseudomonadales; Hastings, M. genomic of. 17-DEC-2002 clone

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RESULT 10
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                                                                                                      DCMB Box 91000
Duke University
Duke University
Curham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   970 GCGCGTCGTGGCATTTCGCTGGCGCGCGAGCTAAACCTGCCGATCGTGTCCATCATCGAC
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1031080C09.y1 C. reinhardtii
Lambda Zap II Chlamydomonas
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefeby, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                  Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                             Contact: Charles Hauser
                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                              Vascular Plants. Project: 1031
                                                                                                                                                                                                                                                                                                                                                                                                                          BI725661.1 GI:15701356
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                                                                                       chauser@duke.edu
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a 320 c
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/db_xref="taxon:287"
/clone="pacs2-164" 3167"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic
organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
                                                                   Location/Qualifiers
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Pred. No. 2.9e-10;
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JOURNAL REFERENCE
                                                            REFERENCE
AUTHORS
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KEYWORDS
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AG247247
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Best Local Similarity
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                                                                         Lotus japonicus
Lotus japonicus
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rnaids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
Sato, S., Nakamura, Y. and Tabata, S. Lotus japonicus TAC End sequences Published Only in Database (2002) 2 (bases 1 to 652)
                                                                                                                                                                                                                                                              Lotus japonicus DNA, clone:LjT20k03_not, AG247247
                                                                                                                                                                                                                        AG247247.1
GSS.
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/clone_lib="C. reinhardtii CC-1690, Stress
), Lambda Zap II"
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Direct Submission
Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute
The First Laboratory for Plant Gene Research; 2-6-7
The First Laboratory for Plant Gene Research, Japan
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:ssatc@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
                                                                                                                                                                                                                   CB977199
CAB47003 IVa Ra D11 Cabernet Sauvignon Berry - CACADA Clone CAB47003 IVa Ra D11 3', mRNA sequence CB977199
                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; Vitaceae; Vitis.
                                         Goes
                                                                                                                                       Vitis vinifera
Vitis vinifera
                                                                                                                                                                                                    CB977199.1 GI:30300405
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGTCGCGTCGGTGCGCATCATGAAGGCGATTCACCGCGCCACAGAGCTGAAACTCCCAC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGTÁTTCCTGTAGCAATTGGGATTATGGÁTTTTGAGTTTATGGGAGGTAGTATGGGAT 131
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                                       da Silva, F., Iandolino, A., Lim, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="LjT20k03_not"
/clone_lib="genomic TAC library"
/note="VECTOR:pYLTAC7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lotus japonicus"
/mol type="genomic DNA"
/strain="Miyakojima MG-20"
/db_xref="taxon:34305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Pred. No. 5.2e-10;
0; Mismatches 219;
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Research; 2-6-7
                                       Baek, J., Jones, K.
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cy - CAB4 Vitis vinifera
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One Shields Ave, Davis, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
Contact: Douglas Cook,
CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: drcook@ucdavis.edu
Seq primer: GCCAAACGAATGGTCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 530 754 6617
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                                                                                                                                                                                                                                                                                                                                                                                                           ATGGGGGGTAGTATGGGATCCGTAGTAGGTGAGAAAATTACCCGTTTGATCGAATATGCC
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                                           GGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCG 609
                                                                                   AGTTTTĞĞTATĞTTĞĞAĞATATCATTATTĞCCĞAACCCAATTCCTACATTĞCATTTĞCĞ
                                                                                                                           TCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCCTG
                                                                                                                                                                                                      GCGCATTTGCCGTTCCTGGTGTATTTGCGCA---ATCCCACGATGGGTGGCGCCATGGCC 489
                                                                                                                                                                                                                                                ACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGGAA 372
                                                                                                                                                                   AATAAAAAGTTATTTTATGTATCAATCCTTACATCTCCTACTACTACTGGTGGGGTGACAGCA
                                                                                                                                                                                                                                                                                      GACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAG 432
                                                                                                                                                                                                                                                                                                                                 ACCAATGAATTTCTACCTCTTATTTTAGTGTGTTCTTCCGGAGGAGCACGTATGCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGGCACAGGTCAACTAAACGGTATTCCCCGTAGCAATTGGGGGTTATGGATTTTCAGTTT
        GGTAAAAGGGTAATTGAACAAACATTGAAAAAGACAGTACCTGAAGGTTCACAAGCGGCT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /(clone lib="Cabernet Sauvignon Berry - CAB4"
//clone lib="Cabernet Sauvignon Berry - CAB4"
//clone lib="Cry, Vector: pDNR, Site 1: Sfil; Site 2:
//clone lib="Cory, Vector: pDNR, Site 1: Sfil; CB44 is a cDNA library of Vitis Vinifera cv.
//cabernet Sauvignon' Clone B berries. Sampled berries were
collected from field-grown vines during stage II of berry
growth (berries were green and hard) at approximately 60
days after full bloom. The average berry size was 9
milimeters. Sampled vines were located at the University
of California, Davis, Experimental Vineyard. CDNAs were
made by oligo-dT priming and directionally cloned. 5'and
3' adaptors were used in cloning as follows:
5'-ARTCTAGAGGCCGAGGCGAGAGTGGCCATTACGGCCGG-3' and
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
91 a 129 c 94 g 203 t
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/gex="HermaphrodIte"
/dev_stage="Berry on stage II,
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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47.8%;
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Pred. No. 2.6e-09;
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Miner, T.,

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AUTHORS
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VERSION
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Best Local Similarity
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   BZ035752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Re 9712, Medical Center Drive, Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat Genome Project: Generation of a Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI229631.1 GI:3813518
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                                                                                                                                                           TGTCGCTGATGCAGATGGCGAAAAACCTCTGCGGCACTGGCAAAAATGCAGGAGCGCGGCT
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                                                                                         TGCCGTACATCTCCGTGCTGACCGACCGACGATGGGCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT773Pac; Site_1: EcoRI; Site_2: 171 c 196 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="ATCC (inhost):2036524"
/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus sp."
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="REMCJ63"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74;
Pred. No.
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   677
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548 TGGGTCCTCGCGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28RPpOT reverse
Class: shotgun
High quality sequence start: 8
High quality sequence stop: 551.
Location/Qualifiers
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Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
n1sta. neh49 row: C column: 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whole genome shotgun reads from Brassica oleracea
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                                CAAGTTTTGGTATGTTGGGGGGATATCATTATTGCCGAACCCTATGCCTACATTGCATTTG
                                                                                                      CAAGTAĀAAAGGTATTCTATATCAATTCTTACATCTCCTACTACCGGTGGGGTGACAG
                                                                                                                                                                                                          AAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCG
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                                                                   CCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTTTCC
                                                                                                                                       AGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAA---TCCCACGATGGGTGGCGCCATGG
                                                                                                                                                                         AAGGAAGTTTAAGTTTGATGCAAATGGCTAAAATTTCTTCGGTTTTATGTGATTATCAAT
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ilarity 47.2%;
Conservative
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/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic DNA"
db_xref="taxon:3712"
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Pred. No. 5.7e-09;
D; Mismatches 283;
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136 TATGCAGAGACCTTGGAGCGGGCTCGAAGCAAGGCCAAATGCGATGAATCGGTAATTACT 195
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; Vitaceae; Vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Mar 14, 2003 this sequence version replaced gi:28967937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAES Genome Facility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tags from cabernet sauvignon
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                                                                    Conservative
                                                                                                                                                                /clone="Cabascono" | Toap Co2"
/sex="Hermaphrodite"
/dev_stage="Veraison"
/lab host="DHSalpha"
/clone lib="Cabernet Sauvignon Berry - CAB2SG"
/clone lib="Cabernet Sauvignon Clone
8 berries Samples were collected at veraison (transition
between stage II and stage III of berry growth) from
field-grown vines 60 days after full bloom. Berries were
still green but soft. Sampled vines were located at the
University of California, Davis, experimental vineyard.
CDNAs were made by oligo-dT priming and directionally
cloned. 5'and 3' adaptors were used in cloning as follows:
5'-ANGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3'
Sonstructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
85 a 102 c 130 g .188 t l others
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                                                                                      5.0%;
                                                                                      Score 73.6; DB 14; Pred. No. 6.2e-09;
                                                                    Mismatches
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                                                                                              CCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAG 612
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                                                                                                                               TTTGGTATGTTGGGAGATATCATTATTGCCGAACCCAATTCCTACATTGCATTTGCGGGT
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TATTTATTCCATAAGGGCTTATTCGATCTAATCGTACCAC
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Search completed: November 13, 2003, 02:26:32 Job time: 3245.57 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Degussa-H1s AG
APPLICANT: Porschungszentrum-Jlich GmbH
APPLICANT: Forschungszentrum-Jlich GmbH
ITILS OF INVENTION: PROCESS FOR THE PREPARATION OF
CURRENT APPLICATION NUMBER: US/09/362,899
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: DE 19924365.4
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2123
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US-09-362-899-1
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Best Local Similarity 100.0%;
Matches 1473; Conservative 0
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LOCATION: (508)..(1980)
OTHER INFORMATION: accDA
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; Sequence 2, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.; APPLICANT: WHITE, Owen R.; APPLICANT: FRASER, Claire M.; APPLICANT: WHOSER, John C.; TITLE OF INVENTION: DNA SEQUENCES FOR ST.; TITLE OF INVENTION: TUBERCULOSIS
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Best Local Similarity
Matches 717; Conserv
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CURRENT APPLICATION NUMBER: US/09/103,
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 2
LENGTH: 4403765
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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US-09-103-840A-1/c
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                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
S-09-103-840A-1
                                                                                                                                                                                                              Query Match 21.2%;
Best Local Similarity 54.0%;
Matches 717; Conservative
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
OGRANISM: Mycobacterium leprae
US-08-311-731A-140
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Patent No. 6583266
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/720-2441 INFORMATION FOR SEQ ID NO: 140:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SMITH, DOU
APPLICANT: MAO, JEN-I
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 36063 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                178 GATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTG
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                                                                                                                                                                                                                                                                                           Similarity
  GCGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGT 357
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                                                    TGCAAATTCAGCTTCCTCGGTGGCCGTATCGGGGTGGCAGCCGCGGAGCGAATCACCGCC 3154
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                                                                                                                                                                                                                                                                     Conservative
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12180
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US-09-252-991A-12180
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PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331-
SEQ ID NO 12180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12180, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1020
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AGCGTCACCGCGAGGCGCATTTGCCGTTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG 478
                                                                                                                                                    CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC 418
                                                                                                                                                                                                                                                            CGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCCTGCTTCCGGTGGTG 358
                                                                                                                                                                                                                                                                                                                 ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGT 238
                                                                                                     CGCGCATGCAGGAAGCGCTGATCTCGCTGATGCAGATGGCCAAGACCTCGGCGGTCCTGG 712
                                                                                                                                                                                                        CAGCCAACGTCGCCCTGGAGAAGCGCTGCCCGCTGATCTGCTTCTCCGCCTCCGGCGCGCG 652
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52.0%;
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Pred. No. 4.2e-23;
0; Mismatches 241;
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31603 ACCCGTATGCAGGAAGGCACCGTCGCGTTCCTGCAGATGGTGAAGATCGCTGCGGCCGTC 31662
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                                                                            CAATTGCGTGCAGCGGTGGCAAAAACCCCTCAAGGTTAT 695
                                                                                                                                                 ATCCAGACAGCGGAGAATCTGCAACGGCATGGGGTAATCGACGCTATCGTCACGCTGGAC 31902
                                                                                                                                                                                                                              ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT 597
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                                                                                                                                                                                                                                                                                                           ATCGGCTTCCTTGGGCCTCGGGTGTATGAGTTGCTGTATGGCGAACCTTTCCCCGTCCGAC 31842
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18 J. Rubenfield et al.
 ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 107196.136 US 60/094,190 Length 1020;

Indels

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RESULT 7
US-09-252-991A-12415/c
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US-09-252-991A-12415
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SEQ ID NO 12415
LENGTH: 1338
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 261;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                             AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG
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                                      TCGGCTTCGCCGGTCCCCGCGTGATCGAGCAGACCGTCCGCGAGAAGCTGCCGGAAGGCT
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ON: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
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CURRENT APPLICATION NUMBER: US/09/773,816
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 60/179,305
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stanford University APPLICANT: Khosla, Chaitan
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TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(23623)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 23673
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                                                                                                                                                     GATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGG 596
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                                      GTTCCAGACCGCCGAATACCTCCTCGAACACGCCTGATCGACCTGATCGTGCCGCGCCC 8138
                                                                        TCTCGGCTTCGCCGGCCGGCGGGTCATCGCGCAGACCATCCGCGAGGAACTGCCGCCGGA
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Pred. No. 2.7e-20;
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CAAAAACCC 685
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RESULT 9
US-09-107-532A-170
US-09-107-532A-170
; Sequence 170, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: OF INVENTION: NUCLEIC ACID
                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7477
                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7537
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    COMPUTER READABLE FORM:
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                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                   CGAGCACTTTGTTGAAGAAATTCTCGGCACAATCAGCAACGCCCTCTCCGA 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGGTCACCGCCCGCGAACTCCTCGGCCTGGGCATCGTCGACGGCGTCCTCCCGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCGTGCAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAAC 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCGCCTCGGCCATCCTCTTCCGCGACACCAACCACGCCGCGAAAATCATAGAGCGACA 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCCCGCCGATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGA 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGCGTGCCGGTCGTCACCGTCGTCACCGGCGAGGGCGCAGCGGCGCGGGGCGCTCGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCCTCCCCACCGTTTCGGTCATTATTGGTCAGGGCGTTGGCGGTGGCGGCTGGCCAT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGAGGAGCAGGCCAGGCCGTCGCCATCGCCGAGAACCTGCGCCTGATGGCGGGCCT 7598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCGCGTGCTGGCGCATTGAGCCCCGGCTGTGCGCGTTGCCCTGGCGCGCATCGGGGGCCCG
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                         COUNTRY: USA
ZIP: 02354
                                                                                      CITY: Waltham
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                                                                                                                                                                                      ENTEROCOCCUS
                                                                                                                                                                                  and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAE
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Best Local Similarity
Matches 247; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 170:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniallo, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...870
SEQUENCE DESCRIPTION: SEQ ID NO: 170:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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ORGANISM: E
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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AATTG 663
                                      TCCAAAAGGCTGAATTCTTATTATCTCATGGTTTTGTCGATCAGATTGTTCCCCGCATGG
                                                                                                                                                      TAGGITICCIGGGICCICGCGIGGIGGAGITAACCACIGGGCAIGCGCITCCAGACGGIG
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                                                                           TCGGTTTTGCTGGAAGACGCGTCATCGAACAGACGATCAAGCAGGAACTTCCAGAAGATT
                                                                                                                                                                                                        GAGTAACTGCCAGTTTTGCAATGGAAGGCGATATTATTCTAGCAGAACCCCAAAGCTTGA
                                                                                                                                                                                                                                              GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAGA
                                                                                                                                                                                                                                                                                     AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/107,532A
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Pred. No. 1.1e-19;
0; Mismatches 238;
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RESULT 11
US-08-961-527-7/c
US-08-961-527-7/c
; Sequence 7, Application US/08961527
; Patent No. 6420135
; Patent No. 6420135
Charles Kunsch
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12365
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
VENTER OF SEQ ID NOS: 33142
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US-09-252-991A-12365/c
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LENGTH: 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12365, Application Patent No. 6551795
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: United Streptococcus
                                                                                                       APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
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          Human Genome Sciences,
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Pred. No. 7.3e-18;
                                                                                                       pneumoniae Polynucleotides and
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Best Local Similarity
Matches 248; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NATA:
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LENGTH: 19702 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Diskett
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APPLICATION NUMBER:
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CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATTCTAACTTTATCATGGCTTCTATGGGTACGGTTGTAGGTGAAAAAATCACTCGTT 11434
                                                                                                                                                                         TAGGTTTCCTGGGTCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG 598
                                                                                                                                                                                                                                                                                                AACGCCATTCAAATGCTGGTCTCTTTTACCTGACCATTTTGACAGATCCAACGACTGGTG 1125
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                                                                                                                                                TTGGTTTTGCTGGGCGTCGTGTGATTGAAAATACGGTTCGTGAAAGCTTGCCTGAGGATT
                                                                                                                                                                                                                       GTGTGACAGCTTCTTTCGCTATGGAAGGCGATATCATTCTGGCTGAACCACAGAGCTTGG 11194
                                                                                                                                                                                                                                                                                                                             AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG 478
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ACTTACCAGATACGATTGCTA 11053
                                    AATTGCGTGCAGCGGTGGCAA 679
                                                                       TCCAAAAGGCAGAATTCCTATTAGAACATGGCTTTGTGGATGCTATTGTCAAAAGAAGAG 11074
                                                                                                           GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAGA 538
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Pred. No. 7.6e-17;
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Best Local Similarity
Matches 248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09557884

Patent No. 6506581

GENERAL INFORMATION:
GENERAL INFORMATION: The Nucleotide sequence of TITLE OF INVENTION: The Haemophilus influenzae Thereof, and Uses Thereof
      1337280
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FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                              239
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GCGTATCAGCCAGTTTTGCGATGTTAGGGGATTTAAATATTGCCCGAGCCAAAAGCCTTAA, 1337339
                                       GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGA, 538
                                                                                                                   AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTG
                                                                                                                                                          CTCGTATGCAGGAAGCATTATTCTCTTTAATGCAAATGGCAAAAACTAGTGCCGTACTTG 1337219
                                                                                                                                                                                               CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC
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TYPE: nucleic acid
STRANDEDNESS: double
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OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3 1/2 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 96.2; DB 4;
Pred. No. 5.7e-16;
0; Mismatches 253;
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US-09-643-990A-1
; Sequence 1, Application
; Patent No. 6528289
; GENERAL INFORMATION:
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                                                                         Query Match
Best Local Similarity
Matches 248; Conserv
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
1336980 AAGATGCGCTAATTACTATGACAGGTACACTTTATAATATGCCAATCGTTGTGGCTGCAT 1337039
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB186P10

TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Robert D. Fleischmann
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                         ATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTGT 238
                                                                                                                                                                                                     LENGTH: 1830121 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3 1/2 inch diskett COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS v6.22 SOPTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                  TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
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                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-Aug-2000 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                           Conservative
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                                                                     Score 96.2; DB 4;
Pred. No. 5.7e-16;
0; Mismatches 253;
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239 CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG 298

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US-09-347-878-25
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                        Matches
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-09-347-878-25
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TITLE OF INVENTION: METHODS AND COMPOSITIONS |
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (1131)...(2399)
COTHER INFORMATION: Escherichia coli nucleic acid encoding
OTHER INFORMATION: folypolyglutamate synthetase-dihydrofolate
OTHER INFORMATION: synthetase
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                                                     TGAPACTCCCACTGCTGGTCTCCCCTGCTTCCGGTGGTGCGCGCATGCAGGAAGACAATC
                                                                                                                       GTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTCACCGCGCCACAGAGC
                                                                                                                                                                                                                                              AAGGCACTCTGTATGGAATGCCGGTTGTCGCTGCGGCATTCGAGTTCGCCTTTATGGGCG
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Pred. No. 2.1e-16;
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CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: PCT/JP97/01043
EARLIER FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: JP 8-97536
EARLIER FILING DATE: 1996-03-28
EARLIER APPLICATION NUMBER: JP 8-146833
EARLIER FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Applic Patent No. 5958706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FINE MAGNETIC PARTICLES CONTAINING USEFUL PROTEINS TITLE OF INVENTION: BOUND THERETO, PROCESS FOR PRODUCING THE SAME, AND TITLE OF INVENTION: THEREOF FILE REFERENCE: MATSUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KAMIYA, Shinji
APPLICANT: NAMBA, Kenryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MATSUNAGA, Tadashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Magnetospirillum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 954
TYPE: DNA
   1011 GATCGTGTCCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGCTCGG 1070
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                                                           RCCNGARGGNTAYMGNAARGCNAARMGNYTNATGGARATGGCNGAYCAYTTYCARGTNCC
                                                                                                                   GCCGCAGGAGCTGCGTTTTGCGCGTCGTGGCATTTCGCTGGCGCGCGAGCTAAACCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCATGGCCTCGTGGGGTT 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTTGCAGCGTCACCGCGAGGCGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACTCCTG 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCGAACAGACCGTTCGCGAAAAAACTGCCGCCTGGATTCCAGCGCAGTGAATTCCTGA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGG 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGGGCGATCTCAACATCGCTGAACCGAAAGCGTTAATGGCTTTGCCGGGTCCGCGTGT 840
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Pred. No. 5.8e-15;
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			CNC	TIG	HYTNTGGMGNWSNGCNGARAAYGCNAARGAYGCNGCNGARCARYTNMGNYTNACNGCNCA	-8 -8 -8	NGTNYTNATGYTNGARCAYGCNATHTAYWSNGTNATHWSNCCNGARGGNTGYGCNWSNAT	GGTCTACGCGGCGAAAAACGCGTGGCCTGTCCGCATTGCCACCAGAGGGCGCCTCGGCCAT	NWSNGTNATHATHGGNGARGGNGGNWSNGGNGGNGCNATHGCNYTNGCNACNGGNAAYAC	ATC	TNG	- 500	GNG-
			RGAYYTNCAYAARYTNWSNATHATHGAYWSNGTNGTNCCNGARCCNATGGGNGGNGCNCA 812	1311 CGCACTTTTAAGCCAAGGGCTTATCGACGGGATCGTCGCCGAAACCGAGCACTTTGTTGA 1370	A 752	CCTCTTCCGCGACACCAACCAGCCGCGGAAATCATAGAGCGACAAGGCGTGCAGGCGCA 1310	T 692		C 632	1131 TICGGICATIATIGGICAGGGCGITGGCGGTGGCGCTGGCCATGCTGCCCGCCGATCT 1190	NCARGCNGARGCNATHGCNMGNWSNATHGARACNTGYYTNAAYGTNMGNGTNCCNYTNGT 572	CATCGCAAGCTCGATTGCGCGCACCTTGTCCAAGCTTATCGACGCTCCCCCTCCCCACCGT 1130	:
			2	370	2	310	92	1250	32	190	72	130	12

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Result
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1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

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17: /cgn2 6/ptodata/2/pubpna/US0 NEW PUB.seq:*

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10 US-09-712-333-35

9 US-09-815-242-7800

9 US-09-815-242-6828

10 US-09-815-242-7288

9 US-09-815-242-7288

10 US-09-815-242-9854

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Sequence 929, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 7800, Ap
Sequence 6828, App
Sequence 97, Appl
Sequence 97, Appl
Sequence 9854, App
Sequence 6133, Ap
Sequence 5520, Ap
Sequence 5521, Ap
Sequence 5521, Ap
Sequence 7115, Ap
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ALIGNMENTS

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US-09-738-626-929
US-09-738-626-929
US-09-738-626-929
Sequence 929, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, MIKIRO
APPLICANT: ANDO, SEIKO
APPLICANT: COCHAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00
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Query Match 100.0%; Score 1473; DB 10; Length 1473; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps

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ATCATCGACACCTCCGGCGCCGAATTGTCGCAGGCGGCTGAGGAGCTCGGCATCGCAAGC
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APPLICANT: ELKMANNS, BERND
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: MOCKEL, BETTINA
ITILE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
ITILE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
ITILE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
ITILE OF INVENTION: ACCDA GENE
ITILE OF INVENTION: ACCDA GENE
ITILE OF INVENTION: ACCDA GENE
ITILE OF INVENTION NUMBER: U010/024,370
CURRENT APPLICATION NUMBER: U09/362,899
PRIOR FILING DATE: 1999-07-29
IPHOR APPLICATION NUMBER: U08/362,899
IPHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1473)
; OTHER INFORMATION: accDA
US-10-024-370-2
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                   GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGGCCATCCTCTTCCGC
                                                      ATTGGTCAGGGCGTTGGCGGTGGCCGCTGGCCATGCTGCCCGCCGATCTGGTCTACGCG
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Sequence 1, Application US/10024370

Publication No. US20020142405A1

GENERAL INFORMATION:

APPLICANT: ELKMANNS, BERND

APPLICANT: EGGELING, LOTHAR

APPLICANT: EGGELING, LOTHAR

APPLICANT: MOCKEL, BETTINA

TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY

TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY

TITLE OF INVENTION: ACCDA GENE

FILE REFERENCE: 21123-284139-MAS

CURRENT APPLICATION NUMBER: US/10/024,370

CURRENT APPLICATION NUMBER: 09/162,899

PRIOR APPLICATION NUMBER: 09/362,899

PRIOR APPLICATION NUMBER: DE 199 24 365.4

PRIOR APPLICATION NUMBER: DE 199 24 365.4

PRIOR FILING DATE: 1999-07-29

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GGCACAATCAGCAACGCCCTCTCCGAATTGGATAACAATCCGGAGAGGGCGGGACGCGAC 1440
                                                                                                                                            GCCGAAAACGCGTGGCTGTCCGCATTGCCACCAGAGGGCGCCTCGGCCATCCTCTTCCGC 1260
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APPLICANT: HAVASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TAYEISHI, NACKO
APPLICANT: TAYEISHI, NACKO
APPLICANT: TAYEISHI, NACKO
APPLICANT: TAYEISHI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: J99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATCHIN ONS: 7059
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, KIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, MAOKO
APPLICANT: TATEISHI, MAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
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ANDO, SEIKO
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US-09-712-363-35
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PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR PILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR PILING DATE: 1999-02-01
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR APPLICATION NUMBER: 60/165,066
PRIOR PILING DATE: 1999-11-12
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Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
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APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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                                                                                               ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA
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Pred. No. 5.5e-87;
0; Mismatches 589;
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Sequence 7800, Application US/09815242
Patent No. US30020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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; NAME/KEY: CDS
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US-09-815-242-7800
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 7800
LENGTH: 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.3%;
Best Local Similarity 52.8%;
Matches 265; Conservative
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
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ORGANISM: Pseudomonas
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RESULT 7 US-09-815-242-6828

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; LOCATION: (1).
US-09-815-242-6828
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 6828
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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ORGANISM: Enterococcus
FEATURE:
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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FILING DATE: 2000-05-26
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ATAGGTTTCCTGGGTCCTCGCGTGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGT 597
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                              GGTGTTACCGCAAGTTTTGCGATGGATGGCGATATTATTTTGGCAGAGCCTCAGAGTTTA
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Pred. No. 3.7e-27;
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RESULT 8
US-09-070-927A-458
(Sequence 458, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
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                                                                                                                                                                                    Query Match
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 6021 base pairs
TYPE: nucleic acid
5381 ATGGACGCTAATTTTATCATGGGAGTATGGGAAACGATTGTTGGTGAAAAAAATCACACGC 5440
                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kenley K. Hoover a REGISTRATION NUMBER: 40,3 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diske
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Patrick J. Dillon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides 
NUMBER OF SEQUENCES: 982
                                                                                                         178 GATGAATCGGTAATTACTGGAGAAGGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTTG 237
                                 238 TCCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAG 297
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OPERATING SYSTEM: MSDOS ve
SOFTWARE: ASCII Text
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ilarity 53.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                309-8504
                                                                                                                                                 0; Mismatches
                                                                                                                                                                Score 121; DB 10;
Pred. No. 7.9e-27;
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PRIOR EILING
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-23
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                                           US-09-815-242-7288
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                                                                                                                                                                                         SEQ ID NO 7288
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR PRIOR DATE: 2000-05-23
PRIOR RILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck,
APPLICANT: Ohlsen, K
APPLICANT: Zyskind,
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                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                  PRIOR FILING
                                                                                                                        LENGTH: 870
TYPE: DNA
ORGANISM: Helicobacter
                                                                 NAME/KEY: CDS
LOCATION: (1)
                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23.
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR FILING DATE: 2000-12-22
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Trawick, John D.
Carr, Grant J.
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Zyskind, Judith W.
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    8.1%;
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      Score 119.2;
      BB
      9;
    Length 870;
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US-09-895-913A-97
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97, Application US/09895913A Patent No. US20020160456A1 GENERAL INFORMATION:
                                                                SEQ ID NO 97
LENGTH: 1053
TYPE: DNA
ORGANISM: Helicobacter
                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                  FILE REFERENCE: 06.12/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
                                                                                                                                                                                                                                                     APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal
                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                FEATURE:
NAME/KEY: CDS
LOCATION: (110)...(976)
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Miller, Charles
Tomb, Jean Francois
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0; Mismatches 273;
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RESULT 11
US-09-815-242-9854
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APPLICANT: Ohlsen, Kai
APPLICANT: Zyskind, Ji
APPLICANT: Wall, Danid
APPLICANT: Trawick, Jo
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Best Local S
Matches 283
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 9854, Application US/09815242 Patent No. US20020061569A1
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
 OR APPLICATION NUMBER: 60/191,078
OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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                                                                                                                                                                                                                                                    Yamamoto, Robert T.
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Pred. No. 1.4e-26;
0; Mismatches 273;
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 9854
LENGTH: 993
TYPE: DNA
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US-09-815-242-6133
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                                                                                                                                        Sequence 6133, Application US/09815242 Patent No. US20020061569A1
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Best Local Similarity 49.6%;
Matches 276; Conservative
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NAME/KEY: CDS
LOCATION: (1).
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 Trawick, John D. Carr, Grant J. Yamamoto, Robert Yamamoto, Robert Yu, H. Howard
                                                                                                                                                                                                                                                                 CGGTGGCAAAAACCCT
                                                                                                                                                                                                                                                                                                                       AGAATTTGGTGAAAACTGGTGTGTATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAG
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Pred. No. 4.5e-23;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEEQ for Windows Version 4.0
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Best Local S
Matches 275
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NAME/KEY: CDS
LOCATION: (1)...(915)
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875
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                                    GCGTGGCACTTCCGGTGATGGA 761
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                                                                            GCATTCTGGCGAAGTTGATGAATCTGCCAGCGCCGAATCCTGAAGCGCCGCGTGAAGGCG
                                                                                                                  AAACCCTCAAGGTTATTCAGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACTCCTG
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TAGTGGTACCCCCGGTACCGGA 896
                                                                                                                                                                                                   TGAAAACTGGTGTGATTGATGGAATTGTGTCGCCACTCCAATTGCGTGCAGCGGTGGCAA 679
                                                                                                                                                                                                                                                                                    TGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGG
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                                                                                                                                                             TCGAGAAAGGCGCGATCGACATGATCGTCCGTCCGGAAATGCGCCTGAAACTGGCGA
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48.9%;
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Pred. No. 1.8e-21;
0; Mismatches 287
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RESULT 13
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CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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Best Local Similarity
Matches 249; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                   512
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                                         GCGCCATGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCCGGCGCGCAGA
                                                                                                                      AGCGTCACCGCGAGGCGCATTTGCCGTTTCCTGGTGTATTTTGCGCAATCCCACGATGGGTG
                                                                                                                                                                                   CCCGTATGCAGGAAGGAATCATGAGTCTCATGCAGATGGCTAAGATCTCTGCGGCGGTTA
                                                                                                                                                                                                                                 CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC
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GTGTGACAGCTTCTTTCGCTATGGAAGGCGATATCATTCTGGCTGAACCACAGAGCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall, Daniel
Trawick, John D.
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Pred. No. 6.6e-20;
0; Mismatches 252;
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LENGTH: 654

TYPE: DNA
ORGANISM: Bacillus clausii
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (654)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 8481
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US-09-974-300-5531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5531, Application Patent No. US20020146721A1 GENERAL INFORMATION:
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Best Local Similarity 51.8%;
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                                                                                                                                                                                                                                                                                                                            CCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTCACC
                                  TGGCCTCGTGGGGTTCATCTGGGCATCTCACTTTTGCGGAACCCGGCGCGCAGATAGGTT
                                                                                                        ACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCACGATGGGTGGCGCCA
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Pred. No. 1.2e-19;
0; Mismatches 264;
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US-09-815-242-7115
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US-09-815-242-7115
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ
SEQ ID NO 7115
                                                                                                                                                                                                                                                                               Query Match 6.5%;
Best Local Similarity 49.5%;
Matches 248; Conservative
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith
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APPLICANT:
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 891
TYPE: DNA
ORGANISM: Haemophilus
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359 CGCGCATGCAGGAAGACAATCGAGCTTTTGTCATGATGGTGTCCATAACCGCGGCTGTGC 418
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                                                                                                                     CGAACTTTGCTTTTATGGGCGGTTCAATGGGTTCTGTAGTTGGTGCAAAATTTGTTAAAG
                                                                                                                                                 CCGATTTTTCCTTCCTCGGCGGTTCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGG
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                                       CGGCTGAAAAAGCGATGGAAATGAATTGTCCATTTGTGTGTTTTCTCTGCGAGTGGTGGTG 499
                                                                             CGATTCACCGCGCCACAGAGCTGAAACTCCCACTGCTGGTCTCCCCCTGCTTCCGGTGGTG 358
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Zyskind, Judith W.
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Pred. No. 2.1e-19;
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AATTGCGTGCAGCGGTGGCAA 679	TGCAGCAGGCGGAGAATTTGGTGAAAACTGGTGTGATGATGGAATTGTGTCGCCACTCC 658	539 TAGGITTCCIGGGTCCICGCGIGGTGGAGTTAACCACTGGGCATGCGCTTCCAGACGGTG 598	GCGCCATGGCCTCGTGGGGTTCATCTGGGGCATCTCACTTTTGCGGAACCCGGCGCGCGC	419 AGCGTCACCGCGAGGCGCATTTGCCGTTCCTGGTGTATTTGCGCAATCCCCACGATGGGTG 478	

Search completed: November 13, 2003, 06:16:54 Job time : 912.783 secs

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Maximum DB
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2448
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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                                                                                                                                                                                                                                                   SUMMARIES
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Enterococcus faeca
H. pylori GHPO 451
Helicobacter pylor
Helicobacter pylor
Salmonella typhi c
                                                                                            C. glutamicum accD
C glutamicum prote
Corynebacterium gl
Mycobacterium cube
                                                                                                                                                                                        Description
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Staphylococcus aur	AAY72365	22	314	11.2	274	-
S. murayamaensis A	P5763	24	526	11.2	275	
Staphylococcus aur	AAU37315	22	314	11.2	275	-
/lococcus	AAU34396	22	309	11.3	277	
ຌ	AAW48309	19	875	•	282	
Staphylococcus	ABP38941	23	315	11.6	283.5	_
S. coelicolor Ac	AAU98725	23	527	•	285	_
Bifidobacter	ABP66186	23	540	11.7	285.5	-
Haemophilus	AAE30458	24	315	11.8	288	-
На	AAU35421	22	315	11.8	288	
Magnetospirullu	AAW27453	18	317	11.8	289	-
S. epidermidis	AAG83050	22	280	11.9	291.5	-
Streptoco	ABP28022	23	256	11.9	291.5	_
Listeria	ABB48047	23	318	12.3	300.5	
	AAB96609	22	527	12.	307	•
Listeria	ABB48048	23	294		318.5	_
Chlamydia	AAY34658	20	255		319.5	_
Pse	AAU36305	22	290	13.	22	_
S. pneumo	ABU00780	24	288		334	_
CFE 67 proteir	AAM01064	22	288	13.	334	•
Streptococcus	AAU38025	22	288	13.	334	•
Streptococcus	AAU37772	22	288	13.	334	
m	ABP28020	23	288	13.	335	_
Staphylococcus aur	92	22	252	13.	4	
	a	22	285	14.	4	•
aphylococcus	2	22	285		4	_
	2	24	292	14.	4	_
	ABP38958	23	293	14.	ũ	-
pidermidis	AAG83049	22	285		354.5	~
Novel human diagno	ABG25523	22	1106	14.	9	٠,
cter [ABU50977	23	279	14.	362	٠.
Protein involved i	689	20	312	14.	364	-
ยน	801	23	291	14.	365	_
mophilus influ	561	22	296	15.	368	
actococcus lacti	6	23	288	15.	368	-
E. coli cellular p	AAU34637	22	304	15.	374	_

ALIGNMENTS

RESULT 1 AAB45789 ID AAB4

AAB45789 standard; Protein; 491 AA

AAB45789;

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WPI; 2001-042411/06.
N-PSDB; AAC82732, AAC82733.
                                   Tilg Y,
                                                                                                                                                 L-amino acid; accDA; coryneform microorganism; L-lysine; animal feed; medicine; pharmaceutical industry.
                                                                        27-MAY-1999;
                                                                                      10-MAY-2000;
                                                                                                      29-NOV-2000
                                                                                                                     EP1055725-A2
                                                                                                                                   Corynebacterium glutamicum.
                                                                                                                                                                                       15-MAR-2001 (first entry)
                                                                                                                                                                         glutamicum
                                                 DEGUSSA-HUELS AG. FORSCHUNGSZENTRUM JUELICH GMBH.
                                  Eggeling L,
                                                                                      2000EP-0109842.
                                                                                                                                                                        accDA protein.
                                                                        99DE-1024365.
                                   Eikmanns
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                                   Sahm
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                                   Moeckel
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Cloned Corynebacterium glutamicum accDA gene useful for producing

Ochiai

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Yokoi

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RESULT 2
AAG90675
ID AAG9
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AC AAG9
XX
AC AAG9
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COSY
KW COSY
KW OSGA
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coryneform bacterium that overexpresses the accDA gene. Coryneform bacteria transformed with (I) so that they overexpress the accDA gene useful for producing L-amino acids, especially L-lysine, which are
 Coryneform bacterium; a organic acid synthesis
                                                C glutamicum
                                                                               26-SEP-2001
                                                                                                                                             AAG90675 standard; Protein; 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                protein fragment SEQ ID NO: 4429.
                                                                              (first
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                 amino acid synthesis; vitamin;
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Pred. No. 7.6e-215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                  GGRPVVLIGQDRRFTLGPQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEELGIAS 360
                                                                                                                  FSPTTPGVALFVMEAIARSRDFQRPGIGEIMETIGADVVKLSGARAGALSPAVRVALARI
                                                                                                                                                                                GFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDR
                                                                                                                                                                                                                                              RMQEDNRAFYMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQI
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    SIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVYAAENAWLSALPPEGASAILFR
                                                                                                 FSPTTPGVALPVMEATARSRDPQRPGTGETMETLGADVVKLSGARAGALSPAVRVALART
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                                   GGRPVVLIGQDRRFTLGPQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEELGIAS
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Senoh A, Ikeda
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Pred. No. 1.4e
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Ozaki A;
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; DB 22; 1.4e-214; 0

491;

Indels Length

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Gaps

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RESULT 3
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XX AAB7
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  (BADI )
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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins we useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum nucleic acids encoding and membrane transport proteins or their portions, identifying C. glutamicum or related bacteria, and transformation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALSPAVRVALARIGGRPVVL
                                                                                                                                                                                                                                                                                                                VALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALSPAVRVALARIGGRPVVL
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IIERQGVQAHALLSQGLIDGIVAETEHFVEEILGTISNALSELDNNPERAGRDSRFTRFE
                        I I ERQGVQAHALLSQGLIDGIVAETEHFVEE ILGTISNALSELDNNPERAGRDSRFTRFE
                                                                                          KLIDAPLPTVSVIIGQGVGGGALAMLPADLVYAAENAWLSALPPEGASAILFRDTNHAAE
                                                                                                                KLIDAPLPTVSVIIGQGVGGGALAMLFADLVYAAENAWLSALPPEGASAILFRDTNHAAE
                                                                                                                                                                                     IGQDRRFTLGPQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEELGIASSIARTLS
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Pred. No. 1.8e-211;
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04-SEP-2001 (first entry)

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polymucleotide sequences AAH51947 - AAH52092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying nucleotide or polypeptide sequence for use as drug targe involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
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01-FEB-2000;
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                                                                                         ARSRDPORPGIGEIMETLGADVVKLSGARAGALSPAVRVALARIGGRPVVLIGQDRRF--
                                                                                                                                         AENLRRHGIIDGVVALDRLRPMLDRALTVLIDAPEPLPA-----POTPAPVPDVPTWDSV
                                                                                                                                                               AENIVKTGVIDGIVSPLOLRAAVAKTLKVI----QPVEATDRFSPTTPGVA--LPVMEAI
                                                                                                                                                                                                                                  NOARLPYLVYLRHPTTGGVFASWGSLGHLTVAEPGALIGFLGPRVYELLYGDPFPSGVQT
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47.8%; Pred. No. 8.6e-87;
ative 73; Mismatches 153;
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to obtain antibodies capable of binding to the express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drig discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU35332 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation is a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                      WPI; 2001-611495/70.
N-PSDB; AAS53191.
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Yamamoto RT,
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                                                                                                                                                                                                                                Example 3; Seq ID No 10925; 511pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                           ELITRA PHARM
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; 2000US-206848P.
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Xu HH;
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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including scute, chronic, and atrophic gastriits, and peptic ulcer diseases, e.g. gastric and ducdenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                       New isolated Helicobacter polynucleotides -
for the diagnosis, prevention and treatment
infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHPO
                                                                                                                                                              Claim 8; Page 738-739;
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01-APR-1997;
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peptic ulcer
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                                                                                                                                                                                                                                                                                                                                                                     Miller C,
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Yamamoto RT,
                                                                                                                                                                                            New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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2000US-242578P.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The

Example

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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     Claim 6; Page 172; 642pp; English
                                                        ulcers in mammals
                                                                              New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                                                  Legrain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                             27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                       21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
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                       N-PSDB; AAS56218.
                                                  WPI; 2001-611495/70.
                                                                                                    Haselbeck R,
Yamamoto RT,
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; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
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   21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
                                                                                                                                                              21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC essential prokaryotic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part CC format directly from WIPO at
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22-DEC-2000;
16-FEB-2001;
                               Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                   ABB54092 standard; Protein; 288
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N-PSDB; AAS52496.
Lactococcus lactis IL1403
                                                               Lactococcus lactis protein accD.
                                                                                                  16-MAY-2002
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                     AVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTLIDSVLDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPV
                                                                                                                                                                                                                                                                                   LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SÍVELGSELEPKDVLKFRDSKKÝKDRLASAQKÉTGÉK-----DALVVMKGTLYGMPV
                                                                                                                                                                                                                                                    LPPGFQRSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPEAP-REGVVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq ID No 10230; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
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                                                                                                (first entry
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 374; DB 22;
Pred. No. 1.3e-25;
9; Mismatches 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 304;
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RESULT 12
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB5621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.
  27-SEP-2001
                          WO200170955-A2
                                                                          Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                                                              Haemophilus influenzae cellular proliferation protein #260.
                                                                                                                                                                    AAU35619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequence useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-043418/06.
                                                                                                                                          14-FEB-2002
                                                                                                                                                                                             AAU35619 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                   QAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVE
                                                                                                                                                                                                                                                                                                            HSNAGLFYITVLTDPTTGGVTASFASLGDIILAEPQSLIGFAGRRVIEQTVRQTLPDDFQ
                                                                                                                                                                                                                                                                                                                                     HREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQ
                                                                                                                                                                                                                                                                                                                                                               STFIMASMGTVVGEKLTRLFEYATTEKLPIIVFTASGGARMQEGIMSLMQMAKTSAAVKR
                                                                                                                                                                                                                                                                                                                                                                                                                VADKDSFVEMFTGIESKNPLDFPGYPEKLAATKARTGLDEAVITGTATIKGQKTALAIMD
                                                                                                                                                                                                                                                                                                                                                                                       FSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                        VLDPDSFISWNETPQYDN-LN-QGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 794;
                                                                                                                                                                                                                                                            KAEFLLNHGFVDAIVKRTELRQKLALLLELHTEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288
                                                  influenzae
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                                                                                                                                                                                             Protein;
                                                                                                                                          entry)
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40.0%; Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368; DB 23;
No. 4.4e-25;
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RESULT 13
ABP28019
ID ABP28
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AC ABP28
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ABP28019;

ABP28019 standard;

Protein; 291

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Matches 81
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent tid not form part
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22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essentigenes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                   of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Seq ID No 11212; 511pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck
                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides for the identification and development of 
ibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-611495/70.
DB; AAS53478.
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 251
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                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                   LDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFS
|:| : : : | | :| | | :| :::!| | !: :|:|
                                ENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSP 243
                                                                 EKGVPFISVLTDPTLGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREKLPEGFORS
                                                                                                EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQA
                                                                                                                                FMGGSMGSVVGAKFVKAAEKAMEMNCPFVCFSASGGARMQEALFSLMQMAKTSAVLAQMR
                                                                                                                                                                 FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR 143
                                                                                                                                                                                                  LEPKDILKFKDLKKYKDRINAAQKETGEK------DALITMTGTLYNMPIVVAASNFA
EFLLEKGAIDMIVKRSEMRQTLASVLS---
                                                                                                                                                                                                                                                                                                                                    296 AA;
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; 2000US-257931P.
; 2001US-269308P.
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2000US-206848P.
2000US-207727P.
2000US-242578P.
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Xu HH;
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                                                                                                                                                                                                                                                                                 15.0%;
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                                                                                                                                                                                                                                                               Score 368; DB 22,
Pred. No. 4.6e-25;
" wismatches 80;
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 -KLTNQPSP
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02-JUL-2002

(first entry)

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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated me meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying streptococcus from the composition of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 3685; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telford J,
Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2001; 2001WO-GB04789
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                                                                                                                                                                                                                                                                                                                                                                                                    Local
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DB; ABN68650.
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                                                                                                                                                                                                                                                                                                                                                                             82;
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INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
VDEDSFEELFTGIETK--DPLNFPNYREKLAATROKTNLDEAVVTGLAKIKGOTTALAIM
                                                                                                                                                                                                                                                                                               RHSNOGLFYLTILTDPTTGGVTASFAMEGDIILAEPOALVGFAGRRVIETTVREDLPEGF
                                                                                                                      RHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGV
                                                                                                                                                                         DSHFIMASMGTVVGEKLTRLFELATEKKLPIVIFTASGGARMQEGIMSLMQMAKVSAAVK
                                                                                                                                                                                                                       DFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMVVSITAAVQ
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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2000GB-0028727.
2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                     Score 365; DB 23;
Pred. No. 8.4e-25;
8; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 291;
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Matches 81
                                                                                                                                                                                                                                                                                                                   AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis, pneumopathy in breast feeding infants, and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 761; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1998;
28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY36893 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bartholinitis; pneumopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paratrachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein involved in intermediate metabolism
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                                                                                                                                                                                                                                      81;
                                                                                                                                                                                                                                                    Similarity
EFLLEHGMIDKVVERKQLKTTLESLL
                           ENLVKTGVIDGIVSPLQLRAAVAKTL 229
                                                       EAKLPYISVLTNPTSGGVTASFASLGDVIIAEPKALICFAGPRVVSQVIGEDLPEGAQKS
                                                                                   EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQA 203
                                                                                                                FMAGSMGAVVGEKLTRLIEKAIDSRLPVIIVSASGGARMQESVFSLMQMAKTSAALAKLH
                                                                                                                                            FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR 143
                                                                                                                                                                           SWNPLFSDLRSQDPLNFVDTDTYPNRLEKARKDNPDSEGVLVGACTIGSYPVALAVMDFS
                                                                                                                                                                                                       SWN----ETPQYDNLN----QGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFS
                                                                                                                                                                                                                                                                                                312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inclusion conjunctivitis; genital
uretritis; epidymitis; cervicitis;
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97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                   Score 364; DB 20;
Pred. No. 1.2e-24;
35; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease; perihepatitis;
                                                                                                                                                                                                                                                              Length 312;
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RESULT 15
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Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein-protein interaction; ulcer; selected interacting domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori selected interacting domain (SID) protein #320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-674910/72.
N-PSDB; ABX65721.
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                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JAN-2001; 2001US-259302P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2002
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                                                                                                                                                                                                                                                                                                                                         identified via protein-protein interactions.

Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to represent an illegible residue.
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 164; 642pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legrain P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYBR-) HYBRIGENICS. (INSP ) INST PASTEUR.
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                                                              174 TSAALNRLSEAKLPFISLLSDPTYGGVSASFAFLGDLIIAEPGAMIGFAGPRVIKQTIGA
                                                                                                                          115 LQ-IWFDFSFMGGSLGSVEXEKIVRAINRAVAKREALLIVSASGGARMQESTYSLMQMAK 173
                                                                                             135
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                                                                                                                                                                                                                                                  ; 88
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                        ALPDGVQQAENLVKTGVIDGIVSPLQLRAAVA------KTLKV 231
DLPEGFOTAEFILEHGLIDMÍVHRKDÍKKTLSDLIAMMTHKTSKI 278
                                                                                                                                             VAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVS 134
                                                                                                                                                                                     IEFLCDVGSFEEFDKHLRPN-DPLNXVDKESYKORIKKYEKRTNRPSSVISGXAKINRMP
                                                                                                                                                                                                                 IDSVLDPDSFISWNE--TPQYDNLN----QGYAETLERARSKAKCDESVITGEGTVEGIP 74
                                                                                           ITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGH 194
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                                                                                                                                                                                                                                                                                                                279
                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                              AA:
                                                                                                                                                                                                                                                 14.8%; Score 362; DB 23; 39.6%; Pred. No. 1.5e-24; tive 40; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Reuse H,
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                                                                                                                                                                                                                                                                                 Length 279;
                                                                                                                                                                                                                                                      Indels 16;
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Search completed: November 13, 2003, 06:40:21 Job time : 80 secs

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Result
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Maximum DB
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     GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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F64838
AD0803
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probable acetyl-Co
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protein
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ALIGNMENTS

RESULT E70783

probable accD3 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: 870783
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S, Connor, R., Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
N.; Julious J.; Julious J

Holroyd, S.

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Qy	dg Qy	g Qy	Qу	Qy dd	Qy db	D Qy	Query Match Best Local Matches 23	A;Status: pre A;Molecule ty A;Residues: 1 A;Cross-refer A;Experimenta C;Genetics: A;Gene: accD3 C;Superfamily
372 APLPTVSVIIGQGVGGGALAMLPADLVYAAENAWLSALPPEGASAILFRDTNHAAEIIER 431	315TLGPQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEELGIASSIARTLSKLID 371 : : : : : : : :	257 ARSRDPORPGIGEIMETLGADVVKLSGARAGALSPAVRVALARIGGRPVVLIGODRRF 314	203 AENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALPVMEAI 256	143 REAHLÞFLVYLRNÞTMGGAMASWGSSGHLTFAEÞGAQIGFLGÞRVVELTTGHALÞDGVQQ 202 	83 SFLGGSLGTVASVRIMKAIHRATELKLÞILVSÞASGGARMQEÐNRAFVMMVSITAAVQRH 142 :	23 SVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDF 82	Query Match 42.8%; Score 1047; DB 2; Length 495; Best Local Similarity 47.8%; Pred. No. 1.2e-57; Matches 233; Conservative 73; Mismatches 153; Indels 28; Gaps 8;	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-495 COL> A;Cross-references: GB:Z73101; GB:AL123456; NID:g3261565; PIDN:CAA97379.1; PID:g1314044 A;Experimental source: strain H37Rv C;Genetice: A;Gene: accD3 C;Superfamily: propionyl-CoA carboxylase beta chain

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RESULT 2
AF3504

C. Accession: AF3504

T. T. Date: 0. Accession: AF3504

C. Accession: AF3504
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AE2101
                                                                                 C;Accession: AE2101
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
B,;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
B;Accession: AE2101
                                                                                                                                                                                                                                  acetyl-CoA carboxylase beta chain [imported] - Nostoc sp. (strai C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
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A;Map position: I
C;Superfamily: acetyl-CoA
C;Keywords: ligase
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
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                  A; Molecule type: DNA
A; Residues: 1-316 < KUR>
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A;Cross-references: GB:AE008917; PIDN:AAL53201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: AD3252; PMID:11756688
A;Accession: AF3504
A;Cross-references: GB:BA000019; PIDN:BAB74063.1; PID:g17131456; GSPDB:GN00179
                                                               A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGVQAHALLSQGLIDGIVAETEHFVEEILG---TISNALSELDN-----NPERAGRDSR 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMLGDIHIAEPGALIGFAGPRVIEQTIREKLPEGFQSSEYLMEHGMVDMVVSRLELKATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELKRPLVLFASSGGARMQEGILSLMQLPRTTVAVEMLKEAGLPYIVVLTNPTTGGVTASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELKLPLLVSPASGGARMQEDNRAFVMVVSITAAVQRHREAHLPFLVYLRNPTMGGAMASW 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIDRIKDYRSRTGMDDAIVNGLGTIEGLPIVATVQDFSFMGGSLGMGAGEAIIQGFEKAI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKTLKVI -- OPVEATDRFSPTTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRAT 105
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43.3%;
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Pred. No. 1e-1
43; Mismatches
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1e-19;
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09-Dec-2002
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RESULT 5
F64638
acetyl-CoA
C;Species:

carboxylase beta subunit Helicobacter pylori

Helicobacter

pylori (strain

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acetyl-coenzyme A carboxylase chain B - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori
A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999

C;Accession: E71875

C;Accession: E71875

C;Accession: E71875

C;Accession: E71875

C;Accession: E71875

C;Accession: E71875

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
[Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; 7

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathor, Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain PCC 7120 C;Genetics:
A;Gene: accD
A;Gene: accD
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AB001518; GB:AE001439; NID:g4155454; PIDN:AAD06468.1; PID:g415546: A;Experimental source: strain J99 C;Genetics: A;Genetics: A;Gene: accD A;Gene: accD C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain
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                                                                                        179 MQMAKTSAALNRLSEAKLÞFISLLSDÞTYGGVSASFAFLGDLIIAEÞGAMIGFAGÞRVIK 238
                                                                                                                                  130 VMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVE 189
                                                                                                                                                                                119 INRMPLQIVVFDFSFMGGSLGSVEGEKIVRAINRAVAKKEALLIVSASGGARMQESTYSL 178
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                                                                                                                                                                                                                                                                            60 NATERIEFLCDVGSFEEFDKHLRPN-DPLNFVDKESYKQRIKKYEKRTNRPSSVISGEAK 118
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87; Conserv
                                                                                                                                                                                                                                                                                                                                                                ch 15.8%; Score 387.5; DB 2; Similarity 39.6%; Pred. No. 5.2e-17; 91; Conservative 43; Mismatches 81;
                                                                                                                                                                                                                                                                                                                  SALTLIDSVLDPDSFISWNE--TPQYDNLN----QGYAETLERARSKAKCDESVITGEGT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLELLVSPASGGARMQEDNRAF 129
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                   LTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVA-----KTLKV 231
QTIGADLPEGFQTAEFLLEHGLIDMIVHRKDLKKTLSDLIAMMTHKTSKI
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Pred. No. 2.8e-17;
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C;Superfamily: a
C;Keywords: liga
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetyl-CoA carboxylase (EC 6.4.1.2) - Salmonella enterica subsp. enterica serovar C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi
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A;Molecule type: DNA
A;Residues: 1-289 <TOM>
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mcson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthe
                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-304 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000604; GB:AE000511; NID:g2314086; PIDN:AAD07995.1; PID:g231408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                               Superfamily: acetyl-CoA carboxylase, Keywords: ligase
                                                                                                                                                                                      Matches
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VAAAFEFAFMGGSMGSVVGARFVRAVEQALEDNCPLVCFSASGGARMQEALMSLMQMAKT
                                       AVILSDESELGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI 135
                                                                                                                                      ALTLIDSVLDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPV
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                                                                                                                                                                                      49;
                                                                                                                                                                                                              Score 375; DB 2;
Pred. No. 3.3e-16;
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Pred. No. 8.6e-17;
                                                                                                                                                                                   Mismatches
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LPPGFQRSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPDAP-REGVVVP
                                              LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP
                                                                                                 SAALAKMQERGLPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK 240
                                                                                                                                                TAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHA 195
  295
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acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase N.Contains: carboxyltransferase beta chain XMECBD Species: Escherichia coli beta chain [validated] Escher

C;Date: 31-Dec-1988 #sequence revision 05-Dec-1997 #text_change 01-Mar-2002 C;Accession: B65004; C29803; B29805; E40637; I41212 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y. N.T.; Burland, V.; Riley, . : ဂ္ဂ

Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B65004

K-12

A;Residues: 1-304 <BLAT> A; Molecule type: DNA A;Status: nucleic acid sequence not shown; translation not

A;Cross-references: GB:AE000320; GB:U00096; NID:g1788647; I A;Experimental source: strain K-12, substrain MG1655 R;Nonet, M.L.; Marvel, C.C.; Tolan, D.R. J. Biol. Chem. 262, 12209-12217, 1987 A;Title: The hisT-purF region of the Escherichia coli K-12 A;Reference number: A29803; MUID:87308226; PMID:3040734 PIDN:AAC75376.1; PID:g1788655

A; Accession: C29803 Identification

PIDN: AAA23965.1;

PID: g146364

A; Experimental source: strain R; Bognar, A.L.; Osborne, C.; S A; Cross-references: GB: M68934; GB
A; Cross-references: GB: M68934; GB A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-75, 'SV', 78-225, 'ALPVRVLSNR', 236-304 <NON>
A; Residues: GB: M68934; GB: J02800; NID: g146359;

R;Bognar, A.L.; Osborne, C.; Shane, B.
J. Biol. Chem. 262, 12337-12343, 1987.
A;Title: Primary structure of the Escherichia coli folc A;Reference number: A29805; MUID:87308246; PMID:3040739
A;Accession: B29805 gene and 118 folylpolyglutamate

A;Molecule type: DNA
A;Residues: 1-224, MALPVRVLSNRPFAK', 240-304 <BOG>
A;Residues: 1-224, MALPVRVLSNRPFAK', 240-304 <BOG>
A;Cross-references: GB:M32445; NID:g146018; PIDN:AAA23807.1;
R;Li, S.J.; Croman Jr., J.E. PID: g146019

J. Bacteriol. 175, 332-340, 1993
A;Title: Growth rate regulation of Escherichia coli acetyl coenzyme A;Reference number: A40637; MUID:93123150; PMID:7678242
A;Accession: E40637 A carboxylase, which

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-32 <LI1>

A;Cross-references: GB:S53037; NID:g263402; PIDN:AAB24894.1; A;Note: sequence extracted from NGBI backbone (NCBIN:122320, R;Bogner, A.L.; Osborne, C.; Shane, B. J. Biol. Chem. 262, 12334-12343, 1987 PID: g263404 NCBIP: 122322)

J. Biol. Chem. 262, 12334-12343, 1987
A;Title: Primary structure of the Escherichia coli
A;Reference number: I41212
A;Accession: I41212 folc gene and its folylpolyglutamate

A;Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-224, 'MALPVRVLSNRPFAK', 240-304 A; Residues: GB: J02808; NID: 9148007; <RES>
PIDN:AAA23801.1; PID:9146008

A; Gene: accD; dedB; usg A; Map position: 50 min

A; Map position: 50 min C; Complex: in E. coli, otin carboxyl carrier protein acetyl-CoA carboxylase is protein (BCCP, homodimer) composed of biotin carboxylase
(PIR:BKEC9) (EC 6.3

A;Pathway: fatty acid biosynthesis C;Function: <CTRB> A;Description: EC 6.4.1.2 [validated, MUID:75035569]; the acetyl-CoA carboxylase

complex

A;Description: catalyzes the transfer of the carboxyl group from the carboxyl-biotin

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C; Superfamily: (C; Keywords: fat) F;27-49/Region:
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-304 <STO>
A;Cross-references: GB:AE005174; NID:g12516675; PIDN:AAG57445.1; GSPDB:GN00145; UWGP:Z35
A;Experimental source: strain O157:H7, substrain EDL933
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acetyl-CoA carboxylase
C;Species: Escherichia
C;Date: 18-Jul-2001 #se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase beta chain [similarity] C;Species: Escherichia coli
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Best Local
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                                                                                                                                                                                                                                                                                                                                                        121 VAAAFEFAFMGGSMGSVVGARFVRAVEQALEDNCPLICFSASGGARMQEALMSLMQMAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 ALTLIDSVLDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                          TAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTLIDSVLDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAALAKMQERGLPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLVELGSELEPKDVLKFRDSKKYKDRLASAQKETGEK-----DALVVMKGTLYGMPV
                                                                                                                                                                                                              LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP 251
                                                                                                                                                                                                                                                               SAALAKMQERGLPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPGFORSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPEAP-REGVVVP
                                                                                                                                                                      LPPGFQRSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPEAP-REGVVVP
                                                                                                                                                                                                                                                                                                                                                                                                     AVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMVVSI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLVELGSELEPKDVLKFRDSKKYKDRLASAQKETGEK-----DALVVMKGTLYGMPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
  #sequence_revision 18-Jul-2001 #text_change 31-Dec-2001
                          coli
                                                (EC 6.4.1.2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 374; DB 2;
Pred. No. 3.8e-16;
                                                  carboxyltransferase beta chain [similarity]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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A;Status Park
A;Nolecule type: DNA
A;Residues: 1-284 <WHI>
A;Cross-references: GB:AE001970;
A;Cross-references: strain R1
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A75422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                         A;Gene: DR1215
A;Map position: 1
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetyl-CoA carboxylase carboxyl transferase, beta subunit - Deinococcus radiodurans C;Species: Deinococcus radiodurans C;Decies: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: A75422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000007; PIDN:BAB36623.1; PID:g13362670; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hayashi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-304 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A75422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Superfamily: acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Accession: H91028
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                                                                                                                                                                    Matches
                                                                                                                                                                                                             Query Match
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Best Local Similarity
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  115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                         70 VEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAF 129
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                                                                                                                                                                    l Similarity
87; Conserv
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  LHGLPVTLAVMDFAFSGGSMGSVVGEEIARAAEYAAESRTPLLLVAASGGARMQESALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPPGFQRSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPEAP-REGVVVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVILSDESFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI 135
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                                                                                                                           SALTLIDSVLDPDSF--ISWNETPQYDNLN----QGYAETLERARSKAKCDESVITGEGT 69
                                                                                    SAERRVEVLADPGSFRQLSGQVHP-VDPLHFTDTEPYPERLRRAQAKTGRPDAILTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii,
Kasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                  Conservative
                                                                                                                                                                                     15.2%;
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                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                                                         GB:AE000513; NID:g6458956; PIDN:AAF10788.1;
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Pred. No. 3.8e-16;
9; Mismatches 92;
                                                                                                                                                                                       Score 372.5;
Pred. No. 4.
                                                                                                                                                                      Mismatches
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                                                                                                                                                                    4.3e-16;
ches 90;
                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                             Length
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M.; Shinagawa,
                                                                                                                                                                                                               284;
                                                                                                                                                                                                                                                        chain
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Ε.ς.
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C.; Mal
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A; PROTECUTE: 1-276 < AQP>
A; Cross-references: GB: AE000690; NID: g2983100;
A; Cross-references: GB: AE000690; NID: g2983100;
                                                     A;Experimental source: strain C;Genetics: C;Genetics: A;Gene: accD C;Superfamily: acetyl-CoA cark
                                                                                                                                                                                                     A;Title: The complete genome A;Reference number: A70300; NA;Accession: F70340
                                                                                                                                                                                                                                                                                                              acetyl-CoA carboxyltransferase beta subunit - Aquifex aeolicus C;Species: Aquifex aeolicus C;Decies: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change C;Accession: F70340
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C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain
                                                                                                                                                                A;Status: preliminary; nucleic acid A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-282 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acetyl-CoA carboxylase transferase C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revis
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                                                     acetyl-CoA carboxylase, carboxyltransferase beta chain
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15.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.1%; Score 370.5; DB 2 36.5%; Pred. No. 5.7e-16; tive 42; Mismatches 85
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 Score
Pred.
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                                                                                                                                                                                    sequence
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369.5; DB 2;
No. 6.4e-16;
                                                                                                                                                                                                                                                                                         T.; Young,
                                                                                                                                                                                    not shown; translation
                                                                                                                            PIDN: AAC06712.1;
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                                                                                                                                                                                                                                       bacterium Aquifex aeolicus
                   Length 276;
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RESULT 13
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C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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                      QAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVE
                                                                                HREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQ
                                                                                                              STFIMASMGTVVGEKLTRLFEYATTEKLPIIVFTASGGARMQEGIMSLMQMAKTSAAVKR
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                                                     HSNAGLFYITVLTDPTTGGVTASFASLGDIILAEPQSLIGFAGRRVIEQTVRQTLPDDFQ
                                                                                                                                          FSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQR
                                                                                                                                                                      VADKDSFVEMFTGIESKNPLDFPGYPEKLAATKARTGLDEAVITGTATIKGQKTALAIMD
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                                                                                                                                                                                                                              Score 368; DB 2;
Pred. No. 8.4e-16;
7; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.; Jaillon,
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acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase beta chain - Haemophilus influe C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 18-Jun-1999
C;Accession: B64113
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M., Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800

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B64113 RESULT 14

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A;Description: the enzyme complex catalyzes the synthesis of malonyl-CoA; the tin bound to BCCP (see BKEC9) with bicarbonate; carboxyltransferase catalyzes A;Pathway: fatty acid biosynthesis A;Note: first committed step C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain C;Keywords: fatty acid biosynthesis; ligase; zinc finger F;29-51/Region: zinc finger CCCC motif
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A;Residues: 1-296 <TIGR>
A;Cross-references: GB:U32806; GB:L42023; NID:g1574717; PIDN:AAC22913.1; PID:g1574718;
A;Note: named as homolog to a protein from Escherichia coli
C;Function:
                                                                                                                                                                                                                                                                                                                                                                             R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, etch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Pohl, T.M.; Portetelle, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Y., M.; Ogawa, K.; Groche, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Aluthorse, Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror A; Mithers, P.; Wipht, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipht, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aluthorse; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Roference number: A69580; MUID:98044033; PMID:9384377
A,Accession. G7001
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A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14881.1; PID:g2635386
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetyl-CoA carboxylase homolog yttI - Bacillus subtilis
C;Species: Bacillus subtilis
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                                                                                                                 A;Gene: yttI
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase beta chain
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84;
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                             14.8%; Score 363; DB 2; 38.2%; Pred. No. 1.5e-15;
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                   GVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEAT 238
                                                                                                                           DFQTAEFLLKHGQLDAVIH----KDDMKKTLENLLDMHQT
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                                                            VQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPD 198
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Search completed: November 13, 2003, 06:45:04 Job time : 39 secs

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         GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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P53003

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O67266

O67266
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Q54776 synechoccc
P08193 escherichia
P43778 haemophilus
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Q57417
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Q9bbs1
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7 brassica na
1 lotus jagon
8 porphyra pu
9 nicotiana t
5 arabidopsis
4 epifagus vi
2 angiopteris
7 spinaciano
9 pinus thunb
3 pisum sativ
7 marchantia
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8 haemophilus
3 chlorella v
7 synechocyst
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	ALI PRT;	ACCA SYNY3 ACCA HELPY ACCA HELPY PCCE RAT ACCA SYNP7 ACCA SYNP7 PCC5 MYCTU ACCA ANTSP PCC6 MYCPU ACCA PORPU PCCB RHOER PCC6 MYCTU ACCA HUMAN
equence update) sequence update) arboxylase carboxyl transfi sta chain). R MTCY31.32C. R MCCBan J., Churche: as S., Barry C.E. III, Tek; as S., Barry C.E. III, Tek; as S., Barry C.E. III, Tek; as S., Chillingworth T., Conn 1.1 T., Gentles S., Hanlin I A., McLean J., Moule S., I M.A., Rajandream M.A., Ro; as Squares S., Squares I M.A., Rajandream M.A., Ro; as Squares S., Squares I M.A., Rajandream M.A., Ro; as Squares S., Squares I M.A., Rajandream M.A., Ro; as Component L., Haft D., mayam L.A., Ermolaeva M.D., idman J., Khouri H., Gill i Mycobacterium tuberculosis S. A COMPONENT OF THE ACETY A COMPONENT OF THE ACETY RIER PROTEIN AND THEN THE 1 ACED / PCCB FAMILY.	ALIGNMENTS RT; 495	ACCA SYNY3 ACCA HELPY ACCA HELPY PCCB RAT ACCA SYNP7 ACCA ANTSP PCCS MYCTU ACCA ANTSP PCCB MYCPLE ACCA PORPU PCCB RHOER PCCB HOER PCCB HOER PCCB HUMAN
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Matches 233
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PRINTS; PR01070; ACCCTRFRASEB.
Hypothetical protein; Fatty acid biosynthesis; Ligase; Complete proteome.
SEQUENCE 495 AA; 51772 Mm.
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InterPro; IPR000438; ACOACC_transfB
InterPro; IPR000022; Carboxyl_trans
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EMBL; AE006979; AAK4
PIR; E70783; E70783.
                                                                                                                               ACCD SYNP7 STANDARD; PRT, 305 AA. 054776; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Acetyl-coenzyme A carboxylase carboxyl transferase (EC 6.4.1.2) (ACCASE beta chain).
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  SEQUENCE FROM N.A.

Phung L.T., Haselkorn R.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

-i-FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZ
-i-CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES
                                                                                          Synechococcus sp. (strain PCC 7942) (Anacystis nidulans Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                               TaxID=1140;
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Pred. No. 1.1e-54;
3; Mismatches 153
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Fatty acid biosynthesis; Ligase; Zinc-finger.
ZN_FING 33 55 C4-TYPE (POTENTIAL)
SEQUENCE FROM N.A.

MEDLINE=87308246; PubMed=3040739;
Bognar A.L., Osborne C., Shane B.;
"Primary structure of the Escherichia coli f
folylpolyglutamate synthetase-dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                    FACED ECOLI STANDARD; PRT; 304 AA.

1908193; 1976937; 1978251;

101-AUG-1988 (Rel. 08, Created)

101-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation)

16-OCT-2001 (Rel. 40, Last annotati
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TIGRFAMS; TIGR00515; accD; 1.
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InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
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                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 83334,
                                                                                                                                                                                                                                                                                                                                                Escherichia coli, and Escherichia coli 0157:H7.
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CATALYTIC ACTIVITY: ATP + acetyl-coa + HCO(3)(-) = ADP + phosphate + malonyl-coa
SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).

SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
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                                                                                                                                                                                                                                                          MEDLINE=21156231; PubMed=11258796;
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                                                                 MEDLINE=91360091;
Nagano Y., Matsuno
                                                                                                                                                               carboxylase, which catalyzes
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                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=0157:H7
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MEDLINE=21074935; PubMed=11206551;
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Blattner F.R., Plunkett G. III, Bloch C.A
Riley M., Collado-Vides J., Glasner J.D.,
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                                                                                                                                                                                                S.J.,
                 ano Y., Matsuno R., Sasaki Y.;
essential gene of Escherichia coli that has
a chloroplast gene of unknown function.";
. Gen. Genet. 228:62-64(1991).
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nce 277:1453-1474(1997).
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091; PubMed=1886618;
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J. Bacteriol. 174:5755-5757(1992).

-i- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CAPALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSCARBOXYLASE CAPALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSCARBOXYLASE THE CARBOXYL GROUP TO FORM MALONYL-COA.

-i- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + nhoenhard - thalonyl-CoA.
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EMBL; J02808; AAA23801.1; -.
EMBL; M68934; AAA23965.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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L; D90862; BAA16165.1; -.
L; D90863; BAA16173.1; -.
L; AE005463; AAC57445.1; -.
3L; AP002561; BAB36623.1; -.
777777, AAB24894.2; -.
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SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
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LPPGFORSEFLIEKGAIDMÍVRRPEMRLKLÁSILAKLMNLPAPNPEAP-REGVVVP
                                              LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP
                                                                                                          SAALAKMQERGLPYISVLTDPTMGGVSASFAMLGDLNIAEPKALIGFAGPRVIEQTVREK
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C4-TYPE (POTENTIAL).
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IGFAGPRVIEQTVRE -> MALPVRVLSNRPFAK (IN REF. 1).
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MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., "Whole."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit
(EC 6.4.1.2) (ACCASE beta chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                  Fatty acid
                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000438; ACOACC transfB
InterPro; IPR000022; Carboxyl_trans
Pfam; PF01039; Carboxyl_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32806; AAC22913.1; -. PIR; B64113; B64113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gan
Pasteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCD OR HI1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P43778;
                                                                                                                                                                                                                                                                                                                    TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; HI1260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01070; ACCCTRFRASEB.
                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + acetyl-CoA' + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY). SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAEIN
   144
                                        131
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                                                                          84
                                                                                                               79
                                                                                                                                                   25
                                                                                                                                                                                       81;
                                                                                                                                                                                                         Similarity
   EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQA
                                        FMGGSMGSVVGAKFVKAAEKAMEMNCPFVCFSASGGARMQEALFSLMQMAKTSAVLAQMR
                                                                        FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR
                                                                                                                 LEPKDILKFKDLKKYKDRINAAQKETGEK-----DALITMTGTLYNMPIVVAASNFA
                                                                                                                                                   LDPDSFISWNETPQY-DNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFS
                                                                                                                                                                                                                                                                                                                    TIGR00515; accD; 1.
                                                                                                                                                                                                                                                            biosynthesis; Ligase; Zinc-finger; Complete proteome
29 51 C4-TYPE (POTENTIAL).
296 AA; 32635 MW; 3FEE316557FD4553 CRC64;
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                       45;
                                                                                                                                                                                                         Score 368; DB 1;
Pred. No. 5.1e-15;
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                                                                                                                                                                                       Indels
                                                                                                                                                                                                                            296;
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RESULT 5
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Best Local Similarity
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P56293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
Tnamura A., Yoshinaga K., Sugiura M.;
"Complete nucleotide sequence of the chloroplast genome from the
green alga Chlorolla vulgaris: the existence of genes possibly
involved in chloroplast division.";
Proc. Natl. Acad. Sci. U.S.A. 94:9567-5972(1997).
-i- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT CARBOXYLASE
INVOLVED IN CHLOROPLAST CARBON METABOLISM.
-i- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01039; Carboxyl trans; PRINTS; PR01070; ACCCTRFRASEB. TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorella vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast ZN_FING 36 58 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB001684; BAA57908.1; -. PIR; T07261; T07261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97303241; PubMed=9159184;
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STRAIN=IAM C-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - !- SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
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AM C-27 / Tamiya;
MYVSITAAVQRHRE-AHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVE
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                                                                                                                                                  EGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFV 130
                                                                                                                                                                                                                SSTERIESLVDANTWRPFDEMVSPCDPLEFRDQKAYTERLKDAQERTGLQDAVQTGTGLL 124
                                                                                                                                                                                                                                                                     SALTLIDSVLDPDSFISWNE----TPQYDNLNQGYAETLERARSKAKCDESVITGEGTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 AA;
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                       60;
                                                                                                                                                                                                                                                                                                                                                             Score 361;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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RESULT 6
ACCD_SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase
(EC 6.4.1.2) (ACCASE beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=92118327; PubMed=1368738;
Coura Y., Yoshida T., Nakamura Y., Tak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCD SY
                                                                                                       EMBL; D10004; BAA00893.1; -.
EMBL; S77740; AAC60398.1; -.
EMBL; D63999; BAA10092.1; -.
PIR; JQ1238; JQ1238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.; Sugiura M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
       Fatty acid biosynthesis;
                                     PRINTS; PR01070; ACCCTRFRASEB.
                                                     InterPro; IPR000438; ACoACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96127529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agric. Biol. Chem. 55:2259-2264(1991).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCC6803."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                          + malonyl-coa.
SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUN OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=8590279;
                       accD;
     Ligase;
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Zinc-finger; Complete proteome
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n Synechocystis
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RESULT 7
ACCD_SOYBN
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Best Local :
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SEQUENCE
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the companies of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Resnik; TISSUE=Leaf; Reverdatto S.V., Beilinson V., Nielsen N.C. "The rps16, accD, psa1, ORF 203, ORF 151, gene cluster in the chloroplast genome of (In) Plant Gene Register PGR95-051
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
16-OCT-2001 (Rel.
SEQUENCE
             Fatty acid biosynthesis; Ligase; Zinc-finger; Cl
ZN_FING 169 191 C4-TYPE (POTENTIAL)
                                                  InterPro; IPR000438; ACOACC_transfB
InterPro; IPR000022; Carboxyl_trans
Pfam; PF01039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
                                                                                                           EMBL; U26948; AAA80643.1; -. PIR; T06341; T06341.
                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                  entities requires a
                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P49158;
                                       TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCD
                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                     FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.4.1.2)
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                                                                                                                                                                                                                                                                             malonyl-CoA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLAQLISLHQP-----FYP----ILPPLNADSNQVNPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFAMLGDLILAEPKATIGFAGRRVIEQTLREKLPDDFQTSEYLLHHGFVDAIVPRPQLKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSYKDRIRDTQKATDLTDAVQTGHGRLDGLPIALGVMDFRFMGGSMGSVVGEKLCRLIEY
                                        TIGR00515; accD;
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326
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33, Last sequence update)
40, Last annotation update)
4 carboxylase carboxyl transferase
CASE beta chain).
           191
48857 MW;
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99177B806671A85B
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4B4256A7496ABDED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432
                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                           N.C.;
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                        Chloroplast.
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                                                                                                                                                                                                                    EMBL outstation
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Query Match

13.6%;

Score 332.5;

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  Query Match
                                         Fatty ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase
(EC 6.4.1.2) (ACCASE beta chain).
                                                                                                                                                                                                                             the
                                                                          PIR; S66564; S66564.
InterPro; IPR000438; ACOACC transfB.
InterPro; IPR000022; Carboxyl trans, pfam; pF01039; Carboxyl trans; 1.
PRINTS; PR01070; ACCCTERRASEB.
                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                         embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                         cloning and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                        Elborough K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Jet neuf;
MEDLINE=96207569; PubMed=8670092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCD_BRANA
P48937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRANA
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                                                                                                                                                                                                                                                                                                                                                                      "Biotin carboxyl carrier protein and carboxyltransferase subunits of
the multi-subunit form of acetyl-CoA carboxylase from Brassica napus
cloning and analysis of expression during oilseed rape
                                                                                                                                                                                                                                                                                                                                                                                                                 Rawsthorne S., Slabas A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3708;
                                                                   TIGRFAM8;
                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + acetyl-CoA + + malonyl-CoA.
                                                                                                                                                                                                                                                                                                                      Chem. J. 315:103-112(1996).
FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produ
sen the Swiss Institute of Bioinformatics
                                                    acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
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                                                                                                                                               Z50868; CAA90747.1; -.
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                                                                                                                                                                                                  non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                       requires a license agreement
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                                                                  TIGR00515; accD;
                            489
                                     biosynthesis; Ligase; Zinc-finger; Chloroplast.
229 248 C4-TYPE (POTENTIAL)
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                           ΑA,
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                           55476 MW;
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  13.5%;
                                                                             trans; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
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2; Mismatches
 Score 331.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                          4-TYPE (POTENTIAL)
540C79FB2A239432
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ches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pphyta; Tracheophyta;
core eudicots; Rosidae;
                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          White A.J.,
Length 489;
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Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Createu,
28-FEB-2003 (Rel. 41, Last sequence upd:
28-FEB-2003 (Rel. 41, Last annotation upd:
28-FEB-2003 (Rel. 41, Last annotation upd:
Acetyl-coenzyme A carboxylase carboxyl
Acetyl-coenzyme A carboxylase chain).
                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a linear and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloroplast.

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Loteae, Lotus.
                                                                                                                   InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
PRNNTS; PR01070; ACCCTRFRASEB.
                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
-!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Accession MG-20;
MEDLINE=21082929; PubMed=11214967;
Kato T., Kaneko T., Sato S., Nakam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCD
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                                                             SEQUENCE
                                                                         Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast ZN_FING 235 257 C4-TYPE (POTENTIAL).
                                                                                                        TIGRFAMs; TIGR00515; accD;
                                                                                                                                                                               EMBL; AP002983; BAB33205.1;
                                                                                                                                                                                                           entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BBS1;
                                                                                                                                                                                                                                                                                                                                                                                                                      japonicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lotus japonicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIPVALGVMDFQFMGGSMGSVVGDKITRLIEYATNQCLPLILVCSSGGARMQEGSLSLMQ
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                                                          501
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                                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato S., Nakamura Y., Tabo of the chloroplast genome
                                                          57038 MW;
             13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.4%;
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Score 330.5; DB 1
Pred. No. 1.5e-12;
2; Mismatches 78
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0; Mismatches
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                                                            C08B8B343D7DE54D
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smatches 82;
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21

IDSVLDPDSFISWN-

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Conservative

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Indels

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                                                                                                    Query Match
Best Local (
                                                                                          Matches
                                                                                                                                                                                           EMBL; U38804; AAC08084.1; -.
PIR; S73119; S73119.
InterPro; IPR000438; ACoACC transfB.
InterPro; IPR000022; Carboxyl trans.
Pfam; PF01039; Carboxyl trans; 1.
                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. Rep. 13:333-335(1995).
- PUNCTION: PROBABLE SUBURIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
- I- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PORPU
                                                                                                                                    Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast ZN FING 34 56 C4-TYPE (POTENTIAL). SEQUENCE 288 AA; 32168 MW; C2FD4C8A04D8E261 CRC64;
                                                                                                                                                                        PRINTS; PR01070; ACCCTRFRASEB. TIGRFAMS; TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Reith M.E., Munholland J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
(EC 6.4.1.2) (ACCASE beta chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Rhodophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloropiast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCD
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
if and this statement is not removed. Usage by an
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                                             98
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                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
QERLPAIILCASGGARMQEGMLSLMQMAKISSALEMHKKENLLYLSVLTSPTTGGVTASF
                   ELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASW
                                            YSQRLKDTAFKTSLQDAVQTGVGTMLGQKVCLGIMDFRFMGGSMGSVVGEKLTRLLEKAT
                                                                  YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDESELGGSLGTVASVRIMKAIHRAT
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                                                                                          Conservative
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                                                                                       13.4%; Score 329; DE 38.6%; Pred. No. 9.76 tive 39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
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RESULT 11
ACCD_TOBAC
ID ACCD_T
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Best Local
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Shinozaki K., Ohme M., Tanaka M., Wakasuya A., Obokata J.,
Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
Matsubayashi T., Ohto C., Torazawa K., Meng B.-Y.,
Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y.,
Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F.,
Deno H., Kamogashira T., Sugiura M.,
Takaiwa F.,
Tanahah N., Shimada H., Sugiura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization and expression."; EMBO J. 5:2043-2049(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
(EC 6.4.1.2) (ACCASE beta chain).
                                                                                                                                                                                                                                                                                 Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast. ZN_FING 247 269 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                    Pfam; PF01039; Carboxyl trans; PRINTS; PR01070; ACCCTRFRASEB. TIGR00515; accD; 1.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z00044; CAA77362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCD OR YCF11 OR ZFPA.
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VAVILSDESELGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVS 134
                                                IELLIDPGTWDPMDEDMVSLDPIEFHSEEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIP
                                                                                                   IDSVLDPDSFISWNETP-----QYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIP
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                                                                                                                                                                                                                                                            512 AA;
                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                            58472 MW;
                                                                                                                                                                           13.3%;
                                                                                                                                                      49;
                                                                                                                                                                              Score 326.5; DB 1; Pred. No. 2.7e-12;
                                                                                                                                                                                                                                                            DFBC3312E6228868 CRC64;
                                                                                                                                                      Mismatches
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                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                    InterPro; IPR000022; Carboxyl trans.

Pfam; PF01039; Carboxyl trans; 1.

PRINTS; PR01070; ACCCTRFRASEB.

TIGRPAMs; TIGR00515; accD; 1.

Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast.

Fatty acid biosynthesis; C4-TYPE (POTENTIAL).

CN_FING 231 250 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000438; ACOACC_transfB.
InterPro; IPR000022; Carboxyl_trans.
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Sato S., Nakamura Y., Kaneko T., Asamizu E., T
"Complete structure of the chloroplast genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCD OR ATCG00500.
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28-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase
(EC 6.4.1.2) (ACCASE beta chain).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress)
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CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phose + malonyl-CoA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARATH
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                                                                                                                                                                                        Similarity
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     GIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVM
                                                   IELSIDPG----TWNPMDEDMVSADPIKFHSKEEPYKNRIDSAQKTTGLTDAVQTGTGQLN
                                                                                                      IDSVLDPDSFISWN-----ETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVE 71
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488 AA;
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                                                                                                                                                                                     Score 324.5;
Pred. No. 3.3
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                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
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                                                                                                                                                                                     .3e-12;
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                                                                                                                                                                                                             DB 1;
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e of Arabidopsis
                                                                                                                                                            82;
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eudicots; Rosidae;
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RESULT 13
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (EC 6.4.1.2) (ACCASE beta chain).
ACCD OR YCFIL OR ZFPA OR DEDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wolfe K.H., Morden C.W., Palmer J.D.;
"Function and evolution of a minimal plastid genome f
nonphotosynthetic parasitic plant.";
Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).
-!- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT
INVOLVED IN CHLOROPLAST CARBON METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMs; TIGR00515; accD; 1.
Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast.
ZN_FING 235 257 C4-TYPE (POTENTIAL).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; lamiids; Lamiales; Orobanchaceae; Orobancheae;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01039; Carboxyl trans; PRINTS; PR01070; ACCCTRFRASEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S78384; S78384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA +
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MEDLINE=93066301; PubMed=1332054;
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16-OCT-2001
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InterPro; IPR000022; Carboxyl trans.
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  ITAAVQRHR-EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTG
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                                                    IAIGVMDFQFMGGSMGSVVGEKITRLIBYATNKILPLIIVCASGGARMQEGSLSLMQMAK
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25, Last sequence up
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                                                                                                                                                                                                                                                                                               Score 323.5; DB 1; pred. No. 3.8e-12;
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PIR; S19230; BWFNZT.

InterPro; IPR000438; ACOACC transfB.

InterPro; IPR000022; Carboxyl trans.

Pfam; PP01039; Carboxyl trans; 1.

PRINTS; PR01070; ACCCTRFRASEB.

TIGRPAMS; TIGR00515; accD; 1.
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01-DEC-1992
01-DEC-1992
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                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoshinaga K., Kubota Y., Ishii T., Wada K.; "Nucleotide sequence of atpB, rbcL, trnR, de genes from a fern Angiopteris lygodifiolia: Spermatophyta lineage before the separation pheridophyta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; E
Filicophyta; Marattiopsida; Marattiales;
                                                                                                                                                                                             Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast ZN_FING 51 73 C4-TYPE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ex
                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 18:79-82(1992).
- i- FUNCTION: PROBABLE SUBURIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.
- i- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
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MEDLINE=92119238; PubMed=1731980;
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16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
(EC 6.4.1.2) (ACCASE beta chain).
ACCD OR YCF11 OR ZFPA OR DEDB.
Angiopteris lygodiifolia (Turnip fern).
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SSVSQIHQVQKKLLYIAVLTYPTTGGVTASFGMLGDIIIAEPKAYIAFAGKRVIEQTLRQ
                    TAAVQRHR-EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGH
                                             ALGVMDFQSMGSVVGEKITRLIEYATQESLPLIIVCASGGARMQEGTLSSMQMAKI
                                                          AVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSI
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314 AA;
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16; Mismatches
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Marattiaceae; Angiopteris
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on of Bryophyta and
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76; Conserv
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InterPro; IPR000438; ACOACC transfB.
InterPro; IPR000022; Carboxyl trans.
Pfam; PF01039; Carboxyl trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
TIGRPAMS; TIGR00515; accD; 1.
Fatty acid biosynthesis; Ligase; Zinc-finger; Chloroplast.
ZN_FING___258___280____C4_TYPE__(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: PROBABLE SUBUNIT OF A BIOTIN-DEPENDENT INVOLVED IN CHLOROPLAST CARBON METABOLISM.

-i- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ400848; CAB88738.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann R.G., Mache R.;
"The plastid chromosome of spinach (Spinacia oleracea): complete nucleotide sequence and gene organization.";
Plant Mol. Biol. 45:307-315(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Geant d'hiver, and cv. 1
MEDLINE=21187424; PubMed=11292076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Caryophyllidae, Caryophyllidae, Chenopodiaceae, Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetyl-coenzyme A carboxylase carboxyl transferase (EC 6.4.1.2) (ACCASE beta chain).
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ELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKV
                                                                                   MOMAKISSVLYDYOSNKKLFYVSILTSPTTGGVTASFGMLGDIIIAEPNAYIAFAGKRVI
                                                                                                                                           VMMVSITAAVQRHREAHLPFLV-YLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVV 188
                                                                                                                                                                                                    LNGIPVAIGVMDFQFMGGSMGSVVGEKITRLIEYASNKFIPLIIVCASGGARMQEGSLSL
                                                                                                                                                                                                                                                         VEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPILVSPASGGARMQEDNRAF 129
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                                                                                                                                                                                                                                                                                                                                                                       IDSVLDPDSFISWNETPQYDNL------NQGYAETLERARSKAKCDESVITGEGT
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40, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58907 MW;
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34.1%; Pred. No. 5.3e-12;
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Db 467 EQTLNKTVPEGSQAAEFLFHKGLFDPIVPRNLLKGVLSELFEL 509
Search completed: November 13, 2003, 06:41:00
Job time : 27 secs

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Result
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8: sp_organelle:*
9: sp_phage:*
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13: sp_vertebrate
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Q93kfl corynebacte
Q8frs8 corynebacte
Q9f6d6 streptomyce
Q910al streptomyce
Q910al streptomyce
Q8fxy7 brucella me
Q8fxy7 brucella su
Q9gcn5 rhizobium 1
Q9gq8 giardia lam
Q8gdq2 heliobacill
Q8yu12 anabaena sp
Q92tc7 rhizobium m
Q9zkq1 helicobacte
Q8die7 synechococc
Q25604 helicobacte
Q8die7 synechococc
Q25604 helicobacte
Q50132 mycobacteri
Q8xfj5 salmonella
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Q8pj30 xanthomonas	180	Q8PJ30	16	295	13.8	338.5	5
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	Q8.	Q8K633	16	288	.4	343	3
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o G	Q9.	Q9CN12	16	304	٠		ï
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agrobacte	Q81	Q8U9U5	16	317		344	8
yersinia	280	QBDOUL	16	356	14.1	45.	37
	Q8	Q8ZD25	16	304		45.	8
	29:	Q9JVD9	16	290	•	45.	35
Q9k0d3 neisseria m	Q9.	Q9K0D3	16	290	14.2	346.5	34
cs66 staphylococ	gg.	Q8CS66	16	285	•	54.	ü
	Q9 ₁	Q9PJ00	16	280	•	55.	32
	Q8:	Q8XXY3	16	290		359	31
$^{\circ}$	80	QBDSP0	16	288	•	360.5	30
chlamydia	Q9 ₇	Q9PKA1	16	283	14.7	361	29
w	29	Q9Z9C3	16	308		5	28
	80	084295	16	308		361.5	27
æ	QB,	QBUJA8	16	298		5	26
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	80	Q8E1K1	16	291	٠	365	24
	gg.	Q8E718	16	291	•	365	23
rga0 fusobacteri	8Q	Q8RGA0	16	304		367	22
2 lactocod	29	Q9CHF2	16	288		368	21
066754 aquifex aeo	90	066754	16	276	5	369.5	8
	Q9.	10	16	282	•	370.5	19
ν15	60	Q9RV15	16	284		72	18
ffh5 escherichia	80	Q8FFH5	16	332		374	7

ALIGNMENTS

Ma B Q	SOWRE		RERE	R R R R R	R 0 0 0 0 G		RESULT Q93KF1 ID Q
Query Match Best Local Similarity Matches 490; Conser	Pfam; PF00039; Callowyl Leans; 1. Pfam; PF00378; ECH; 1. PRINTS; PR01070; ACCCTRFRASEB. Ligase; Transferase; Complete proteome Ligase; Transferase; S2238 MW; 53D1887	EMBL; X17592; CAC42827.1; EMBL; AP005276; BAB98224.1; InterPro; IPR000438; ACOACC tr InterPro; IPR000022; Carboxyl InterPro; IPR001753; EnCOA hyd Dfan: DF01030; Carboxyl	UENCE AIN=ATO agawa of mplete mitted	SEQUENCE FROM N.A. STRAIN=ATCC 13032; Kim K., Peters-Wendisch Submitted (JUN-1998) to	ACCDA OR CGL0831. Corynebacterium g Bacteria, Actinob Corynebacterineae NCBI_TaxID=1718;	Q93KF1; 01-DEC-2001 01-DEC-2001 01-MAR-2003 Putative ca (Acetyl-CoA	ILT 1 CF1 Q93KF1
vat	78; ECH; 1. 1070; ACCCTF insferase; Cc	EMBL; X17592; CAC42827.1; EMBL; AP005276; BAB98224.1; InterPro; IPR000438; ACOACC transfB. InterPro; IPR000022; Carboxyl trans. InterPro; IPR001753; EnCOA hydrtse.	FROM N.A. S; S; Senomic sequence of Corynebacterium (MAY-2002) to the EMBL/GenBank/DDBJ	SEQUENCE FROM N.A. STRAIN=ATCC 13032; STRAIN=ATCC Hendisch Kim K., Peters-Wendisch Submitted (JUN-1998) to [2]	ACCDA OK CGL0831. COrynebacterium glutamicum (Brevibacterium flavum). Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium. COBI_TaxID=1718;	039XF1; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 23, Last annotation update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Putative carboxyltransferase subunit of acetyl-CoA carboxylase Putative Carboxylase beta subunit) (EC 6.4.1.2).	PRELIMINARY;
9*; 8*; 1	1. CTRFRASEB Complete 52238 MW;	24.1; COACC trboxyl	1 20300 ence of	P.G.	cum (E la; Act mebact	19, C 19, I 23, I erase beta	<i>:</i>
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STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Kawarabayasi Y., Yamazaki J., Itoh T., Yamagishi A., Nisi Usuda Y., Sugimoto S.;

"The entire genomic sequence of Corynebacterium efficiens Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

SUBMITTANSFERASE; Complete proteome

Transferase; Complete proteome

Transferase; Complete proteome

SPOUENCE 483 AA; 51545 MW; 653BA89519BBBDC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Q8FR58; PRELIMINARY; PRT; 483 AA.
Q8FR58; Q1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative carboxyltransferase subunit of acetyl-CoA carboxylase.
ACCDA OR CE0907.
                                                                                                                                                                                                                                                                                                    Corynebacterineae; Corynebacteriaceae; NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                              Corynebacterium efficiens.
Bacteria; Actinobacteridae; Actinomycetales;
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                                          MTRTSARDLIDQVLDKDSFCFWDTPPEYGEIDDDYREALARAREKSGVDEAVITGEGTVE
                                                             MEHTSALTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDR
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                                                                                              Conservative
                                                                                                            62.4%;
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                                                                                              62;
                                                                                              Score 1527.5;
Pred. No. 2.2e-
62; Mismatches
                                                                                                                                                                                                                                                                                                                 Corynebacterium.
                                                                                              115;
                                                                                                                         DB 16; Length
                                                                                              Indels
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Best Local S
Matches 175
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Pfam; PF03255; ACCA; 1.
Pfam; PF01039; Carboxyl trans; 1
PRINTS; PR01069; ACCCTRFRASEA.
PRINTS; PR01070; ACCCTRFRASEB.
TICRFAMS; TICR00515; accD; 1.
SEQUENCE 578 AA; 60667 MM; 9
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O9F6D6;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=20517899; PubMed=10931852;
Marti T., Hu Z., Pohl N.L., Shah A.N., Khosla C.;
"Cloning, Nucleotide Sequence, and Heterologous Expression of Biosynthetic Gene Cluster for R1128, a Non-steroidal Estrogen Antagonist. Insights into an Unusual Priming Mechanism.";
J. Biol. Chem. 275:33443-33448 (2000).
EMBL; AF293442; AAG30193.1; -.
InterPro; IPR001095; AC-COA_CarboxylA.
InterPro; IPR000438; ACOACC transfB.
InterPro; IPR000438; ACOACC transfB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces sp. R1128.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=140437;
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     SITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTG
                                                                                                                                                     LDQLLDPGSAEPIRNDVRTFDVL--GFTDTKPYPARLAAARAATGLDEAVVIVTGRIHGQ 109
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                                                   PLVVAAMDFAFLGGSLGGAVGELITLAAETALAEHLPLLIVSASGGARMQEGAVALMQMA
                                                                                                 PVAVILSDESFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMV
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16,
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Pred. No. 7.9e
71; Mismatches
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Last sequence update)
Last annotation update)
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Q9L0A1;
01-OCT-2000
             STRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Chen C.W., Collins M.,

Loronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Submitted (APR-2000)
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Streptomycineae; Streptomycetaceae; Streptomyces
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H., Hopwood D.A.;
of ordered cosmids and a detailed
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e EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

STRAIN=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular path Brucella melitensis.";
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                            Bacteria; Proteobacteria;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                     Brucella melitensis.
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InterPro; IPR000438; ACOACC transfB
InterPro; IPR000022; Carboxyl trans
Pfam; PF01039; Carboxyl trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
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Nature 417:141-147(2002)
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Pred. No. 7.9e-7
57; Mismatches
                                                                                                                                                                                                                                                                    Created)
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                                                                  Mujer C., Lo
                pathogen
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                                                       Goltsman
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                                          J. -J
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STRAIN=1330 / Biovar 1;

MEDLINE=2247741; PubMed=12271122;

MEDLINE=22247741; PubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.

Paulsen I.T., Seshadri R., Nelson K.E., Kolonay J.F., Madupu R.,

Daugherry S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Paulsen W.C., Ayodeji B., Krani M., Shetty J., Malek J., Van Aken S.

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

"The Brucella suis genome reveals fundamental similarities betweer animal and plant pathogens and symbionts.";

Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8FXY7;
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                                                                                                                                                                                                                                             TIGR; BR2107; -.
Transferase; Complete proteome.
Transferase; Applete proteome.
Transferase; Applete proteome.
Transferase; Applete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brucella suis.
Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyl-CoA carboxylase, carboxyl transferase, beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0515; accD; 1.
PROSITE; PS01159; WW_DOMAIN_1; 1.
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EMBL; AE009634; AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCD OR BR2107.
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  106 ELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASW
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B 301 AA; 33269 MW; BCB69B33AEA8D566 CRC64;
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                                                  YIDRLKDYRSRTGMDDAIVNGLGTIEGLPIVATVQDFSFMGGSLGMGAGEATIQGFEKAI
                                                                                                       YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRAT 105
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43.3%; Pred. No. 3.5e
tive 43; Mismatches
                                                                                                                                                                                17.6%;
43.3%;
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                                                                                                                                                         Score 431.5; DB 1
Pred. No. 3.5e-18;
43; Mismatches 69
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InterPro; IPR000022; Carboxyl trans.
InterPro; IPR0010202; WM Rsp5_WMP.
Pfam; PF01039; Carboxyl trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyl-CoA carboxylase carboxyltransferase beta chain
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PROSITE; PS01159; WM DOMAIN 1; 1.

Transferase; Ligase; Complete proteome
SEQUENCE 308 AA; 34219 MW; 5FBE6E7/
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Takeuchi C., Yamada M., Tabata S.;
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MAFF303099
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q98CN5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      VLDPLKFRD-----EKRYTDRLKDAKAKTGLEDAIVNALGTIEGLPVVVTVQDFA
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                                                                                                                           BYLMEHGMVDMVVSRLEMRQTIARLLKMLKMPGEQK--PLEPEILPPAV
                                                                                                                                                                             ENLVKTGVIDGIVSPLOLRAAVAKTLKVIOPVEATDRFSPTTPGVALPVMEAIARSRDPO 263
                                                                                                                                                                                                                                    <u>EAGLPYIVVLTNPTTGGVTASYAMLGDVHIAEPGALIGFAGPRVIEQTIREKLPDGFQRS</u>
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Pred. No. 6.6e-18;
6; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A putative Acetyl-CoA Carboxylase/Pyruvate Carboxylase fus
in the amitochondriate protist, Giardia lambila.";
L Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF207740; AAG35712.1; -
R InterPro; IPR001095; AC-CoA carboxyla.
R InterPro; IPR000089; Biotin lipoyl.
R InterPro; IPR000089; Biotin lipoyl.
R InterPro; IPR000089; Carboxyl trans.
R InterPro; IPR000022; Carboxyl trans.
R InterPro; IPR000891; HMGL-like.
R InterPro; IPR000891; PYC_OADA.
R Ffam; PF00364; biotin lipoyl; 1.
R Pfam; PF00364; biotin lipoyl; 1.
R Pfam; PF00363; RMGL-like; 1.
R Pfam; PF00363; RMGL-like; 1.
R Pfam; PF00436; PYC_OADA; 1.
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PRINTS; PR01070; ACCCTRFRASEB.
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Giardia lamblia (Giardia i
Giardota; Diplomonadida;
NCBI TaxID=5741;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
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01-MAR-2001
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                                                                                                                 SPEGAASILOPSVYR--NNTAEMRANFISDAELLAHVQRCYPIDLRNAGVVNDIIVGPEY
                                                                                                                                                   PPEGASAIL----FRDTNHAAEI----IERQGVQAHA-----LLSQGLIDGIVAETEH
                                                                                                                                                                                           SPEAEEQCQSRAISECLLAFQAVHVPIISIITGEGGSGGALALAGGNYVGILSKAFYNVI
                                                                                                                                                                                                                           $QAAEELGIASS;ARTĻSKLIDAPLPTV$VIIGQGVGGGALAMLPADLVYAAENAWLSAL
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                                                                                                                                                                                                                                                                                                      ARIGGR-PVVLIGODRRFTLGPOS-----LRFARRGISLARELNLPIVSIIDTSGAEL
                                                                                                                                                                                                                                                                                                                                            HGAEVDTEDAFLVQDAFVYRDARNVTRPQPCDYLKNF-----VDMAASLRVDKCITVAF
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                     PRELIMINARY;
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Pred. No. 6.1e-16;
                     PRT;
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Watanabe A., Iriguchi M., Ishikawa A., Kishida Y., Kohara M., Matsumoto M., Ishimpo S., Sugimoto M., Nakazaki N., Shimpo S., Sugimoto M., Yasuda M., Tabata S.; "Complete genomic sequence of the fil cyanobacterium Anabaena sp. strain PC DNA Res 8:205-213(2001).

EMBL, AP003589, BAB74063.1; --
EMBL, AP003589, BAB74063.1; --
InterPro; IPR000438, ACOACC transfB.
                                                                                                                                                                                                                                                                                                                                                                                                              Q8YUI2;
Q8YUI2;
01-MAR-2002
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
Acetyl-CoA carboxylase beta
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
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Gerdes S., Kyrpides N., Overbeek
Submitted (AUG-2002) to the EMBL;
EMBL; AY142924; AAN87528.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
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                                                                                                                                                                 E=21595285; PubMed=11759840;
T., Nakamura Y., Wolk C.P., Kuri
be A., Iriguchi M., Ishikawa A.,
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nilarity 41.5%;
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Pred. No. 1.3e-
40; Mismatches
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                                                                                             filamentous
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                                                                        224
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Takazawa M.,
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Muraki A.,
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Matches 87
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A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

"Sinorhizobium meliloti strain 1021.";

"Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

R EMBL, AL591782, CAC41417.1;

R InterPro, IPR000022; Carboxyl_trans.

R Pfam; PF01039; Carboxyl_trans.

R Pfam; PF01039; Carboxyl_trans.

R Pfam; PF01039; Carboxyl_trans.
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092TC7; PRELIMINARY; PRT; 304 AA.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21396507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable acetyl-coenzyme A carboxylase carboxyl transferase beta protein (EC 6.4.1.2).
ACCD OR R00030 OR SMC02764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 316 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263
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                                                                                                                                                                                         Similarity
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                              ELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASW
        AEKCPLVMFPASGGARMQEGILSLMQLPRTTVALNMLKEAGLPYIVVLTNPTTGGVTASY
                                                                                 YSDRLRDSRAKTELEDTIVAGLGQVQGIKLVAVAHEFNFIGGSLGIAAGEAIVKAFERAI
                                                                                                                          YAETLERARSKAKCDESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAEDLLKHGFVDDIVPRTQLKNTLSQLIALHQPV------PTTPPMVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWR--PMDENLRATDPLQFRDRKAYSDRLREMEDKLGLLDAVKTGLGQINSSPVALAVMD
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                                                                                                                                                                                                                                                       AA; 33567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35455 MW;
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                                                                                                                                                                 15.9%; Score 389.5; DB 16; 39.2%; Pred. No. 1.1e-15; tive 44; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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Pred. No. 7.9
                                                                                                                                                                                                                                                     4FCC45B674D068AB CRC64;
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QBDIE7; PRELIMINARY;
QBDIE7; QBDIE7;
O1-MAR-2003 (TrEMBLrel. 23, L
O1-MAR-2003 (TrEMBLrel. 23, L
O1-MAR-2003 (TrEMBLrel. 23, L
Acetyl-CoA carboxylase beta s
ACCD OR TLR1643.
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RESULT 12
Q9ZKQ1
ID Q9ZKÇ
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MEDINE-99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.
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01-MAY-1999
01-MAY-1999
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01-MAY-1999 (TYEMBLYE1. 10, Last sequence update)
01-UN-2002 (TYEMBLYE1. 21, Last annotation updat
Acetyl-coenzyme A carboxylase subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Epsilonproteobacteria; Campylobacterales,
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=85963;
13
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                       QTIGADLPEGFQTAEFLLEHGLIDMIVHRKDLKKTLSDLIAMMTHKTSKI
                                                                                                                                   MQMAKTSAALNRLSEAKLPFISLLSDPTYGGVSASFAFLGDLIIAEPGAMIGFAGPRVIK
                                                                                                                                                                    VMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVE
                                                                                                                                                                                                        INRMPLQIVVFDFSFMGGSLGSVEGEKIVRAINRAVAKKEALLIVSASGGARMQESTYSL
                                                                                                                                                                                                                                         VEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAF
                                                                                                                                                                                                                                                                                                                    SALTLIDSVLDPDSFISWNE--TPQYDNLN----QGYAETLERARSKAKCDESVITGEGT
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                                                                                            LTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVA-----
                                                                                                                                                                                                                                                                                NATERIEFLCDVGSFEEFDKHLRPN-DPLNFVDKESYKQRIKKYEKRTNRPSSVISGEAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                  32567 MW; 43B6EAAEB878E630 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          39.6%;
                                                                                                                                                                                                                                                                                                                                                                                            15.8%;
                                                                                                                                                                                                                                                                                                                                                         43; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Score 387.5; DB 16;
Pred. No. 1.4e-15;
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Last sequence update)
Last annotation update)

Created)

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RESULT 14
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Best Local S
Matches 94
                                                                                                                      STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhoù L., Kirkness E.F., Peterson S.,

Nelson K., Quackenbush J., Dodson R., Khalak H.G., Glodek A.,

MCKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                      pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria;
Helicobacteraceae; Helicobacter.
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01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
Acetyl-CoA carboxylase beta
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                                                                                                           Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=210;
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                                                                         "The complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura Y., Kaneko T., Sato S., Ikeuch
Watanabe A., Iriguchi M., Kawashima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
MEDLINE=22225144; PubMed=12240834;
Sato S., Ikeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res.
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AE000604; AAD07995.1;
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AP005374; BAC09195.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARMQEGMLSLMQMAKTAAALERHRSAGLLYIPILTHPTAGGVTASFAMLGDIIIAEPKAT
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Last annotation update)
subunit (ACCD).
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Pred. No. 1.9e-15;
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                                                                            pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Nakazaki N.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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Matches 87
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Best Local S
Matches 84
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InterPro; IPR000022; Carboxyl_trans.
Pfam; PF01039; Carboxyl_trans; 1.
PRINTS; PR01070; ACCCTRFRASEB.
SEQUENCE 201 AA; 21323 MW; EF45B
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q50132;
Q50132;
01-NOV-1996
01-NOV-1996
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Smith D.R.;
                                                                                                                                                                                                                                               EMBL; U15184; AAA63045.1; -.
InterPro; IPR000438; ACOACC
                                                                                                                                                                                                                                                                       Robison K.;
Submitted (SEP-1994) to the
                                                                                                                                                                                                                                                                                                                         Submitted (APR-1995)
                                                                                                                                                                                                                                                                                                                                                                       Corynebacterineae;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae.
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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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InterPro; IPR000022; Carboxyl
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                                                                                                                                                            Similarity
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                       SPT----TPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALSPAVRVAL
                                                             FLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRF 241
                                                                                               MQEGTVAFLQMVKIAAAVKLSKRAGLPYLGYLRNPTTGGVFASWGSLGHVTVAEPGVLIG
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IPTPQRPEPIPDVPAWNSVMGSRRPERPSVAQVLRHGATDRVLLSGPGHGEAATTL-LAL
                                                                                                                    MQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIG
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                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                Actinobacteridae; Actinomycetales;
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Last
                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
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                                                                                                                                                          Score 379;
Pred. No. 2.
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Pred. No. :
                                                                                                                                                                                                EF45B8DCBB804FB4 CRC64;
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A57ADDAF34B0AF1C
                                                                                                                                             Mismatches
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                                                                                                                                                                     Length 201;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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Maximum DB
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           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         354.5
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2: /cgn2_6/ptcdatta/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdatta/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/BCTUS_COMB.pep:*
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   SUMMARIES
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Compugen Ltd.
Sequence 3, Appli
Sequence 3803, App
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Sequence 317, Ap
Sequence 11, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 12, Appl
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Sequence 512, Appl
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Sequence 2122, Appl
Sequence 21, Appl
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Sequence 21, Appl
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Sequence 5584, Ap
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Sequence 5584, Ap
Sequence 5797, Ap
Sequence 5786, Ap
Sequence 5786, Ap
Sequence 6531, Ap
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361 STARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVYAAENAWLSALPPEGASAILFR 420	301 GGRPVVLIGQDRRFTLGPQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEELGIAS 360 		121 RMQEDNRAFYMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQI 180	61 ESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGA 120 	1 VEKRPPIMVWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCD 60 	/ Match 100.0%; Score 2448; DB 4; Length 491; Local Similarity 100.0%; Pred. No. 3.5e-242; nes 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 3, Application US/09362899 Sequence 3, Application US/09362899 Patent No. 6361986 GENERAL INFORMATION: APPLICANT: Degussa-H1s AG APPLICANT: POTSCHUNGSZENTTUM-J11Ch GmbH TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY FERMENTATION INTERPREPARATION OF L-AMINO ACIDS BY FERMENTATION FOR THE PREPARATION OF L-AMINO ACIDS BY FERMENTATION INTERPREPARATION ALIGNMENTS	143.5 5.9 5215 3 US-09-105-537-2 128.5 5.2 391 4 US-09-252-991A-24230 Sequence 24230, A 126.5 5.2 2254 2 US-08-677-010-3 126.5 5.2 2254 2 US-08-677-010-3 126.5 5.2 2254 2 US-08-919-3 127 5.0 51 1 US-08-19-33 Sequence 3, Appli 128 5.0 3201 4 US-08-311-731A-411 Sequence 41, Appl 129 5.0 3201 4 US-09-320-879-15 120 4.9 3739 3 US-09-105-537-3 121 4.9 3739 3 US-09-105-537-3 121 4.9 3739 3 US-09-105-537-3 121 4.9 3739 4 US-09-105-537-6 121 4.9 3739 3 US-09-105-537-6 121 4.9 3739 4 US-09-105-537-6 121 4.9 3739 4 US-09-105-537-6 121 4.9 3739 4 US-09-105-537-6 121 4.9 3739 4 US-09-105-537-6 121 4.9 3739 4 US-09-105-537-6 122 4.9 3739 4 US-09-105-537-6 123 4.9 3739 4 US-09-105-537-6 124 9 3739 4 US-09-105-537-6 125 4.9 4550 2 US-08-804-227C-14 119.5 4	

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Sequence 410, Application US/08311731A; Patent No. 6583266; GENERAL INFORMATION:
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                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1215 amino acid
                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SMITH, DOUGLAS
APPLICANT: MGO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                  112 LVSPASGGARMQEDNRAFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHL 171
 288
                                  125
                                                                232 IQPVEATDRFSPT----TPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAG 287
                                                                                                                                 172 TFAEPGAQIGFLGPRVVELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKV 231
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                                                                                                                                                                                                                                      94;
                                                                                                                                                                  5 LVSPSSDGTRMQEGTVAFLQMVKIAAAVKLSKRAGLPYLGYLRNPTTGGVFASWGSLGHV 64
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ALSPAVRVALARIGGRPVVLIGQDRR 313
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                                 IADV---PKLIPTPQRPEPIPDVPAWNSVMGSRRPERPSVAQVLRHGATDRVLLSGPGHG 181
                                                                                                   TVAEPGVLIGFLGPRVYELLYGEPFPSDIQTAENLQRHGVIDAIVTLDGLQLTLNRALIM 124
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nilarity 45.6%;
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US-09-107-532A-3824
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Sequence 3824, Application:
Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
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US-09-134-001C-3803
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SEQ ID NO 3803
LENGTH: 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 638037
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AKLDGÍQYGVAVMDARFRMGSMGSVVGEKÍCRIÍDYCTEHRLÞFILFSÁSGGÁRMÓEGII 183
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                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
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Pred. No. 6.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORPORATION
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                                                                                                                                                                             ; LENGTH: 300
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5240
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                                                                                                                                                                                                                                                                                                                               Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GENERICON: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                            Matches
                                                                                                                                                                                                                                                         SEQ ID NO 5240
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5240,
                                                                                                                                                Query Match
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO. 3824:
SEQUENCE CHARACTERISTICS:
                                                                                                                               Local
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LOCATION: (B) LOCATION 1...289
SEQUENCE DESCRIPTION: SEQ ID NO: 3824:
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 VLDPDSFISWNET------PQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIP
                                                                                                                             Similarity
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Similarity 35.5%;
SFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRH 142
                                                                    SVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAVILSDF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELPEDFQKAEFILSHGFVDQIVPRMELKQKIHTLIEL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGH 194
                                  SAKDPLKFVD-----SKPYPDRMREAQTKTGETEALIAMQGNLNGVDMIACAFEF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I SAAVKRHSNEGLEYLTVLTDPTTGGVTASFAMEGDIILAEPOSLIGFAGRRVIEQTIKO
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                                                                                                            Conservative
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                                                                                                          13.5%; Score 331; DB 4; Length 300; 36.6%; Pred. No. 1.7e-25; tive 37; Mismatches 83; Indels
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Pred. No. 7e-28;
Pred. marches 79; Indels
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US-09-198-452A-76
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US-09-252-991A-28751
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; LENGTH: 339
; TYPE: PRT
                                                                 FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 76
LENGTH: 255
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/09198452P Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28751, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and TITLE OF INVENTION: thereof and uses thereof, in particular further of invention: and treatment of infection
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
ORGANISM: Chlamydia pneumoniae FEATURE:
                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 EAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 LEPVDRLKFRDSKKYKDRLAAAQKDTGÉK-----DALIAMSGKLQGMPVVACAFEFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHR 143
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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US-08-973-275-1
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; ORGANISM: Magnetospirillum AMB-1
US-08-973-275-1
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CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: PCT/JP97/01043
EARLIER FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: JP 8-97536
EARLIER APPLICATION NUMBER: JP 8-97536
EARLIER FILING DATE: 1996-03-28
EARLIER APPLICATION NUMBER: JP 8-146833
EARLIER FILING DATE: 1996-05-16
NUMBER: OF SEQ ID NOS: 6
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MATSUNAGA, Tao
APPLICANT: KAMIYA, Shinj
APPLICANT: NAMBA, Kenryo
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TYPE: PR
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LOCATION:
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No. 595870
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                                                                                                      LSPAVRVALARIGGRPVVLIGQDR-----RFTLG---PQELRFARRGISLARELNLP
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IITLVDTAGAYPGVDAEARGQAEAIARSIETCLNVRVPLVSVIIGEGGSGGAIALATGNT 211
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Pred. No. 3.8e-21;
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Pred. No. 2e-24;
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US-09-328-352-8167
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                                  PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3786
LENGTH: 315
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LENGTH: 279
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                                                                                                                                                                FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
ORGANISM: Staphylococcus epidermidis
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Pred. No. 6.2e-21;
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                                                                                                                                                                                                                                                      AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HT.
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RESULT 11
US-09-107-532A-4837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4837, Applicat
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 84;
                                                                                                                                                                     TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 4837:
                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION UMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                         LENGTH: 262 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                          ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 AENAWLSALPPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIV-----AETEH 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 EVQALSIKKMFLKHLNELNQLTPEELAND-RFEKFRKI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 IIDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVYA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AVRVALARIGGRPVVLIGQD------RRFTLG-PQELRFARRGISLARELNLPIVS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 | QPVEATDRESPTTPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVE--EILGTISNALSELDN-NPERAGRDSRFTRFERL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENSTYSVISPEGAAALLWKDSNLAQIAAETMKITALDLLDLGIIDEVINEPLGGAQKDE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIDTKGAYPGKAAEERGQSESIAKNIMEMASLTVPVIAVVIGEGGSGGALGIGISNRVLM, 213
      ORGANISM: Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIGGIGYLDGKSVTVIGQQRGKDTKDNIYRNFGMAHPEGYRKALRLMKQAEKFNRPIFT 153
                                                                                                                                                                                                               TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09107532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 283.5; DB 4;
Pred. No. 1.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUT
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 433, Application US/09198452A PATENT NO. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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LOCATION: (B) LOCATION 1...262
SEQUENCE DESCRIPTION: SEQ ID NO: 4837:
304 FIIQEWLRLKDLAIEEL--
                                                                                                                    410 PPEGASAILFRDTNHAABIIERQGVQAHALLSQGLIDGIVAE-----
                                                                                                                                                                                                      350 SQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVYAAENAWLSAL 409
                                                                                                                                                                                                                                                  124 QGQRFVLIGQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLAEKFGLPVVFLVDTPGAYP 183
                                                                                                                                                                                                                                                                                     301 GGRPVVLIGQD------RRF-TLGPQELRFARRGISLARELNLPIVSIIDTSGAEL 349
                                       454 HFVEEILGTISNALSELDNNPERAGRDSRFTRFERL 489
                                                                                                                                                                184 GLTAEERGOGWAIAKNLFELSRLATPVIIVVIGEGCSGGALGMAVGDSVAMLEHSYYSVI 243
                                                                                                                                                                                                                                                                                                                                                                           241 FSPTTPGVALPVMEAIARSRDPQRPGIGEIMETLGADVVKLSGARAGALSPAVRVALARI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                          81;
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                                                                             SPEGCASILWKDPKKNSEAASMLKWHGENLKQFGIIDTVIKEPIGGAHHDPALVYSNVRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIGIQKGRDLQENIRRNFGSPHPEGYRKALRLMKQAEKFNRPVITLINTAGAYCGVGAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIG-----QDRRFTLG---PQELRFARRGISLARELNLPIVSIIDTSGAELSQAAEE
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29.4%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%; Score 265.5; DB 4; 29.3%; Pred. No. 1.1e-18; ive 40; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Mismatches
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L.7e-19;
hes 93;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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US-08-611-107-12
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-611-107-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (512) 7. 12:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE TARACTERISTICS:
TENGTH: 327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US SN 07/956,700 FILING DATE: 02-OCT-1992 PRIOR APPLICATION NUMBER: US PCT/US93/0934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USES TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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AAENAWLSALPPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIVA------
                                   TFIDTPGAYAGVSAEELGQGEAIAVNLREMFRFSVPILCTVIGEGGSGGALGIGVGDRLL
                                                                                                           LALVGGVGALDGQPVVFLGHQKGRDTKDNVLRNFGMASPGGYRKALRLMEHADRFGMPIL
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                                                                                                                                                                                                                                                                                                                                              10.3%; Score 252.5;
25.2%; Pred. No. 2.2
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US-08-422-560A-12
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Best Local Similarity
Matches 86; Conserv
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
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APPLICATION NUMBER: US 0
FILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 14-APR-199
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselkorn, Rober APPLICANT: Gornicki, Piotr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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400 AAENAWLSALPPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIVA---
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                                 TFIDTPGAYAGVSAEELGOGEAIAVNLREMFRFSVPILCTVIGEGGSGGALGIGVGDRLL 221
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                                                                                                        LALVGGVGALDGOPVVFLGHQKGRDTKDNVLRNFGMASPGGYRKALRLMEHADRFGMPIL 161
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02-OCT-1992
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METHODS FOR
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Pred. No. 2.2
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-793-12
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US-08-468-793-12
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REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEEX: 79-0924
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 86; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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FILING DATE: 30-SEP-1993
CLASSIFICATION: 800
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                                                                       231 VIQPVEATDRESETTEGVALEVMEAIARSEDEOREGIGEIMETLGADVVKLSGARAGALS 290
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-----RRFTL-GPQELRFARRGISLARELNLPIV 339
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                                                                            AAENAWLSALPPEGASAILFRDTNHAAEIIERQGVQAHALLSQGLIDGIVA------
                                                                                                                  TFIDTPGAYAGVSAEELGQGEAIAVNLREMFRFSVPILCTVIGEGGSGGALGIGVGDRLL 221
                                                                                                                                              SIIDTSGAELSQAAEELGIASSIARTLSKLIDAPLPTVSVIIGQGVGGGALAMLPADLVY 399
PLETAQSLRQVL---LRHLKDLQALSPAQLREQRYQKFRQL 319
                           --ETEHFVEEILGTISNALSELDNNPERAGRDSRFTRFERL 489
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Search completed: November 13, 2003, 06:58:22 Job time : 32 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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343.5
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/pubpaa/US09A PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US090 NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10D PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
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       GenCore version 5.1.6 (c) 1993 - 2003 Compugen
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                 14 US-10-024-370-3
10 US-09-738-626-4429
10 US-09-712-363-181
15 US-10-156-761-1252
9 US-09-815-242-11985
9 US-09-815-242-11952
9 US-09-815-242-11212
9 US-09-815-242-11212
9 US-09-815-242-12219
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Sequence 3, Appli
Sequence 1429, Ap
Sequence 181, Ap
Sequence 13252, A
Sequence 10925, A
Sequence 11985, A
Sequence 98, Apl
Sequence 13952, Apl
Sequence 11230, A
Sequence 11212, A
Sequence 11212, A
Sequence 12618, A
Sequence 13618, A
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190.5	190.5	207.5	215.5	217.5	218.5	241	249.5	252.5	252.5	254	257	257	\mathbf{L}	261.5	265	265.5	266	268.5	268.5	268.5	269	270	275	275	277	285	286	288	291
7.8	7.8	•	٠	٠	8.9	9.8	10.2	10.3	10.3	10.4	10.5	10.5	10.7	10.7	10.8	10.8			11.0		11.0	11.0	11.2	11.2	11.3		11.7		11.9
563	563	543	543	593	532	537	316	327	324	516	312	312	484	484	262	324	319	514	255	255	319	266	526	314	309	527	531	315	532
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US-10-205-823-254	US-10-224-539A-10	US-10-259-648-2	US-09-738-626-4285	US-10-224-539A-12	US-10-156-761-11401	US-09-738-626-4284	US-09-815-242-11934		US-09-841-132-566	US-09-738-626-6665	US-09-815-242-11511	US-09-815-242-11339	US-10-106-698-5893	US-09-925-301-1140	US-09-815-242-10926	US-09-841-132-496	US-09-815-242-10048	US-10-156-761-9840	US-09-815-242-13619	US-09-815-242-13366	US-09-815-242-13897	US-09-815-242-4964	US-10-187-267A-47	12-129	42-58	-10-045-	US-10-156-761-10240	09-815-242-11014	US-10-156-761-10868
Sequence 254, App	10	'n	e 42	e 12, Ap		e 4284,	119		566, Ar	e 6665,	1151	1133	e 589:	1140		496,	1004	ce 984	Sequence 13619, A	1336	1389	4964	e 47,	1290	5892	31,	e 10240,	1014, A	Sequence 10868, A

ALIGNMENTS

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TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-024-370-3
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US-10-024-370-3
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APPLICANT: TILG, YVONNE
APPLICANT: ELKNANNS, BERND
APPLICANT: EGGELING, LOTHAR
APPLICANT: SAHM, HERMANN
                                                                                                                                                          Query Match 100.0%; Score 2448; DB 14; Best Local Similarity 100.0%; Pred. No. 1.1e-217; Matches 491; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10024370 Publication No. US20020142405A1
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MOCKEL, BETTINA
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY
TITLE OF INVENTION: PROCESS FOR THE PILE PRICE 21123-284139-MAS
CURRENT APPLICATION NUMBER: US/10/024,370
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/362,899
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: DE 199 24 365.4
PRIOR PILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
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                                                                  ESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLFLLVSPASGGA .120
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                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-4429
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US-09-738-626-4429
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENTIN VEX: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
                                                                                                                                                                                                                          SEQ ID NO 4429
LENGTH: 491
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                                                                                                             Matches
                                                                                                                           Query Match
Best Local Similarity
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                                                             1 VEKRFPTMVWGMEHTSALTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCD
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             ESVITGEGTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGA 120
                                          MEKRF PTMVWGMEHTSALTLIDSVLDPDSF1SWNETPQYDNLNQGYAETLERARSKAKCD
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TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                             Conservative
                                                                                                                           99.9%;
                                                                                                        Score 2445; DB 10;
Pred. No. 2e-217;
1; Mismatches 0;
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          Query Match
Best Local Similarity
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; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-181
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CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
FRIOR APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-01-28
FRIOR APPLICATION NUMBER: 60/179,531
FRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
FRIOR APPLICATION NUMBER: 60/117,844
FRIOR APPLICATION NUMBER: 60/118,206,
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
FRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-712-363-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 181, Applic Patent No. US2002016 GENERAL INFORMATION:
                                                                                                  SOFTWARE: FastSEQ
SEQ ID NO 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROTSTEIN, SETGIO H.
APPLICANT: MARCOTTE, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Eisenberg, David
                                                                                                                                                        NUMBER OF SEQ ID NOS: 292
                                                                             LENGTH:
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20020164588A1
                                                                                                                                  for Windows
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42.8%;

Score 1047; DB 10; Pred. No. 4.5e-88;

Length 495;

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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13252
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                                                                                                                                           ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-13252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13252, Application US/10156761 Publication No. US20030119018A1
                                                                        Matches
                                                                                                          Query Match
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APPLICANT: IKEDA, HARUO
                                                                                                                                                                                             ENGTH: 465
                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 REAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQC
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                                                                                         Similarity
                  LTLIDSVLDPDSFISWNETPQYDNLNQGYAETLERARSKAKCDESVITGEGTVEGIPVAV
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 LPVAEGAYAPDGPLSW-----
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                                                                        Conservative
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                                                                   19.9%; Score 487.5; DB 15; 29.9%; Pred. No. 2.4e-36; tive 66; Mismatches 208;
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 QGYDASRARATERTGEDESVVCGRARIDGTPAVL
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; ORGANISM: Enterococcus
US-09-815-242-10925
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Query Match 16.3%; Score 400; DB 9; Length 288; Best Local Similarity 42.6%; Pred. No. 1.4e-28; Matches 89; Conservative 39; Mismatches 79; Indels
                                                                                                                                                                     SOFTWARE: FASTSEQ
SEQ ID NO 10925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10925, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-12-22
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SOFTWARE: FRATSEQ for Windows Version
SEQ ID NO 11385
LENGTH: 289
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                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-12-22
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                            146 HLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRVVELTTGHALPDGVQQAEN 205
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                                                                                                    GGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNRAFVMMVSITAAVQRHREA 145
                                                                                                                                  DPLNFVD-----KESYKORIKKYEKRTNRPSSVISGEAKINRMPLQIVVFDFSFM
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 KLPFISLLSDPTYGGVSASFAFLGDLIIAEPGAMIGFAGPRVIKQTIGADLPEGFQTAEF
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Xu, H. Howard
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Zyskind, Judith W.
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                                                               APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essent
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13952, Application US/09815242 Patent No. US20020061569A1
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Best Local :
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
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TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel H
TITLE OF INVENTION: Genome
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TYPE: PRT
ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Tomb, Jean Francois
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RESULT 9
US-09-815-242-10230
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                                       CURRENT APPLICATION NUMBER: US/09/815,24:
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
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PRIOR PILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10230, Application Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H.:Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith V
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FILING DATE:
                      FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSPTTPGVALP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAAAFEFAFMGGSMGSVVGARFVRAVEQALEDNCPLVCFSASGGARMQEALMSLMQMAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPPGFORSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNLPAPNPDAP-REGVVVP 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr, Grant J.
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; ORGANISM: Haemophilus influenzae US-09-815-242-11212
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11212
Query Match 15.0%; Score 368; DB 9; 1
Best Local Similarity 36.8%; Pred. No. 1.3e-25;
Matches 81; Conservative 45; Mismatches 80;
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10230
LENGTH: 304
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Best Local Similarity
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
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                                                                                                                                         LENGTH: 296
TYPE: PRT
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Yamamoto, Robert
Xu, H. Howard
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                                        Length 296;
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US-09-815-242-12618
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Best Local Similarity
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Staphylococcus aureus
-09-815-242-12618
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SOFTWARE: FastSEQ for Windows Version
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PRIOR
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APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judi
APPLICANT: Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 285
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OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR FILING DATE: 2000-12-22
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                        128 AFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRV 187
176
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                                                                                                                                                                                                              13 EHTSALTL---IDSVLDPDSFISWNETPQYDN-LN-QGYAETLERARSKAKCDESVITGE
                                                                                                                                                                                                                                                        82;
                                                                                                            GTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMQEDNR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENLVKTGVIDGIVSPLQLRAAVAKTLKVIQPVEATDRFSP 243
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                                                                                                                                                                    DHHIALTAYKRIEAISDEGSFTEFDKGMTSANPLDFPSYIEKIEKDQQKTGLKEAVVTGT
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SLMOMGKTSVSLKRHSDAGLLYISYLTHPTTGGVSASFASVGDINLSEPKALIGFAGRRV
                                                                                  AQLDGMKFGVAVMDSRFRMGSMGSVIGEKICRIIDYCTENRLPFILFSASGGARMQEGII
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Trawick, John D.
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Zyskind, Judith W.
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36.0%; Pred. No. 2.3e-23;
tive 47; Mismatches 94
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US-09-815-242-5424
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SEQ ID NO 5424
LENGTH: 252
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Best Local Similarity
Matches 81; Conserv
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FILE REFERENCE: BLITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                               188
                                                                                         147
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  207
                                                                                                                                   128 AFVMMVSITAAVQRHREAHLPFLVYLRNPTMGGAMASWGSSGHLTFAEPGAQIGFLGPRV 187
                                                                                                                                                                                87 AQLDGMKFGVAVMDSRFRMGSMGSVIGEKICRIIDYCTENRLPFILFSASGGARMQEGII 146
                                                                                                                                                                                                                                                                            27 DHHIÀLTAYKRIEAISDEGSFTEFDKGMTSANPLDFPSYIEKIEKDQQKTGLKEAVVTGT 86
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                                          VELTTGHALPDGVQQAENLVKTGVIDGIVSPLQLRAAVAKTLKVIQ 233
                                                                                         SLMQMGKTSVSLKRHSDÅGLLYISYLTHPTTGGVSÅSFASVGDINLSEPKÅLIGFAGRRV
                                                                                                                                                                                                                          GTVEGIPVAVILSDFSFLGGSLGTVASVRIMKAIHRATELKLPLLVSPASGGARMOEDNR 127
IEQTINEKLPDDFQTAEFLLEHGQLDKVVHRNDMRQTLSEILKIHQ
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Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                     13.9%;
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RESULT 13 US-09-815-242-13365

Sequence 13365, Application U Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.

Application US/09815242

APPLICANT: APPLICANT:

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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Grant J.
APPLICANT: Carr, Grant J.
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SEQ ID NO 13365
LENGTH: 288
                     APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yu. Howard
TITLE OF INVENTION: Identification of Ess
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILLING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2001-02-16
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FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 GYOKKLASMREKTGLHEAVVTGTALIKGOTVALGIMDSNFIMASMGTVVGEKITRLFEYA
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73; Conserv
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39.0%; Pred. No. 1.8e-22;
tive 36; Mismatches 78;
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                                  APPLICANT: Yamamoto, Robert T.
APPLICANT: YAM, H. Howard
ITITLE OF INVENTION: Identification of Essential Ger
ITITLE OF INVENTION: Identification of Essential Ger
ITITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/296,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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US-09-815-242-11898
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PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11898, Application US/09815242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith i
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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               APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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Zyskind, Judith W.
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